

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:39:44 ; Search time 16 Seconds
(without alignments)
951.430 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARRSQRGRGRRGEPCTAL.....PWAHLKAAPLTYFGLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 248812 seqs, 61136040 residues

al number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	249	10	US-09-905-810-2
2	1268	100.0	249	10	US-09-782-980-44
3	1066	84.1	273	10	US-09-742-454A-2
4	1066	84.1	273	10	US-09-883-777-2
5	1020	80.4	225	10	US-09-905-810-1
6	116	9.1	409	10	US-09-813-329-6
7	105.5	8.3	406	10	US-09-813-329-4
8	104	8.2	409	10	US-09-813-329-2
9	92.5	7.3	208	10	US-09-027-287-39
10	92.5	7.3	208	10	US-09-252-656B-39
11	91.5	7.2	240	9	US-09-967-604-6
12	91.5	7.2	240	9	US-10-151-882-45
13	91.5	7.2	240	10	US-09-027-287-2
14	91.5	7.2	240	10	US-09-252-656B-2
15	91.5	7.2	240	12	US-10-066-209-4
16	90	7.1	660	12	US-10-115-178-1
17	88	6.9	373	9	US-10-174-590-372
18	88	6.9	373	9	US-10-176-759-372
19	88	6.9	373	9	US-10-175-737-372

20	88	6.9	373	9	US-10-173-706-372	Sequence 372, App
21	88	6.9	373	9	US-10-175-738-372	Sequence 372, App
22	88	6.9	373	9	US-10-175-752-372	Sequence 372, App
23	88	6.9	373	9	US-10-176-482-372	Sequence 372, App
24	88	6.9	373	9	US-10-176-757-372	Sequence 372, App
25	88	6.9	373	9	US-10-176-913-372	Sequence 372, App
26	88	6.9	373	9	US-10-180-552-372	Sequence 372, App
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32	88	6.9	373	9	US-10-174-588-372	Sequence 372, App
33	88	6.9	373	9	US-10-175-739-372	Sequence 372, App
34	88	6.9	373	9	US-10-175-740-372	Sequence 372, App
35	88	6.9	373	9	US-10-175-743-372	Sequence 372, App
36	88	6.9	373	9	US-10-176-488-372	Sequence 372, App
37	88	6.9	373	9	US-10-176-492-372	Sequence 372, App
38	88	6.9	373	9	US-10-176-747-372	Sequence 372, App
39	88	6.9	373	9	US-10-176-750-372	Sequence 372, App
40	88	6.9	373	9	US-10-176-985-372	Sequence 372, App
41	88	6.9	373	9	US-10-176-987-372	Sequence 372, App
42	88	6.9	373	9	US-10-176-991-372	Sequence 372, App
43	88	6.9	373	9	US-10-176-992-372	Sequence 372, App
44	88	6.9	373	9	US-10-176-993-372	Sequence 372, App
45	88	6.9	373	9	US-10-184-658-372	Sequence 372, App

ALIGNMENTS

RESULT 1

US-09-905-810-2

; Sequence 2, Application US/09905810

; Patent No. US20020015703A1

; GENERAL INFORMATION: 372

; APPLICANT: BIOGEN, INC.

; TITLE OF INVENTION: Antagonists of Tweak and of Tweak

; TITLE OF INVENTION: Receptor and Their Use to Treat Immunological Disorders

; FILE REFERENCE: A068 US

; CURRENT APPLICATION NUMBER: US/09/905,810

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: PCT/US00/01044

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/116,168

; PRIOR FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-09-905-810-2

Query Match 100.0%; Score 1268; DB 10; Length 249;

Best Local Similarity 100.0%; Pred. No. 6.4e-108;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARRSQRGRGRRGEPCTALLVPLALGLALACGLLLAVVSLGSRASLSAQEPAGEEL 60

Db 1 MAARRSQRGRGRRGEPCTALLVPLALGLALACGLLLAVVSLGSRASLSAQEPAGEEL 60

Qy 61 VAEDQDPSELNPOTESQOPAPFLNLRPRRSAPKGRKTRARRAJAAHYEVHPRQCD 120

Db 61 VAEDQDPSELNPOTESQOPAPFLNLRPRRSAPKGRKTRARRAJAAHYEVHPRQCD 120

Qy 121 GAQAGVDTGTVSGWEAEARINSSPLRYNRQICEFIVTRAGLYLYLCQVHFDGKAVYLKLD 180

Db 121 GAQAGVDTGTVSGWEAEARINSSPLRYNRQICEFIVTRAGLYLYLCQVHFDGKAVYLKLD 180

Qy 181 LLVDGVIALRCLEFSTATASSLGQFURLQCVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240

Db 181 LLVDGVIALRCLEFSTATASSLGQFURLQCVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240

Db 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPQSSLRIRTLPAWHLKAAPFL 240

Qy 241 TYFGLFQVH 249

Db 241 TYFGLFQVH 249

RESULT 2

US-09-782-980-44

; Sequence 44, Application US/09782980

; Patent No. US20020072089A1

; GENERAL INFORMATION:

; APPLICANT: Khodadoust, Mehran M.

; APPLICANT: MacBeth, Kyle J.

; APPLICANT: Busfield, Samantha J.

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Gu, Wei

; APPLICANT: White, David

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND

; TITLE OF INVENTION: STMT PROTEIN AND NUCLEIC ACID MOLECULES AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: MNI-121CP

; CURRENT APPLICATION NUMBER: US/09/782,980

; CURRENT FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: PCT/US00/02125

; PRIOR FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: 09/448,076

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 09/276,400

; PRIOR FILING DATE: 1999-03-25

; PRIOR APPLICATION NUMBER: 60/117,580

; PRIOR FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: 09/014,195

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: 09/014,348

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: 09/086,892

; PRIOR FILING DATE: 1998-05-29

; PRIOR APPLICATION NUMBER: 09/296,208

; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: 09/063,950

; PRIOR FILING DATE: 1998-04-21

; PRIOR APPLICATION NUMBER: 09/561,381

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/561,810

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/087,121

; PRIOR FILING DATE: 1998-05-29

; PRIOR APPLICATION NUMBER: 09/672,721

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 09/049,799

; PRIOR FILING DATE: 1998-03-27

; NUMBER OF SEQ ID NOS: 176

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-782-980-44

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Best Local Similarity 100.0%; Pred. No. 6.4e-108;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAARSQRRRRGRRGPGTALLVPLALGLALACLGLLAVVSLGSRASLSAQEPAQBEL 60

Qy 61 VAEEDQDPSLNPQTEESQDPAPFLNRLVRRPSSAPKGRKTRARAAIAAHYVHPRPGD 120

Db 61 VAEEDQDPSLNPQTEESQDPAPFLNRLVRRPSSAPKGRKTRARAAIAAHYVHPRPGD 120

Qy 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCYVHFDEGKAVYIKLD 180

Db 121 GAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCYVHFDEGKAVYIKLD 180

Qy 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPQSSLRIRTLPAWHLKAAPFL 240

Db 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPQSSLRIRTLPAWHLKAAPFL 240

Qy 241 TYFGLFQVH 249

Db 241 TYFGLFQVH 249

RESULT 3

US-09-742-454A-2

; Sequence 2, Application US/09742454A

; Patent No. US20020041876A1

; GENERAL INFORMATION:

; APPLICANT: WILEY, Steven R.

; TITLE OF INVENTION: TWEAK Receptor

; FILE REFERENCE: 2968-B

; CURRENT APPLICATION NUMBER: US/09/742,454A

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: 60/203,347

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 273

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK

; OTHER INFORMATION: fusion protein construct

US-09-742-454A-2

Query Match 84.1%; Score 1066; DB 10; Length 273;

Best Local Similarity 100.0%; Pred. No. 1.8e-89;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 SLGSRASLSAQEPAQEELVAEEDQDPSLNPQTEESQDPAPFLNRLVRRPSSAPKGRKTR 102

Db 67 SLGSRASLSAQEPAQEELVAEEDQDPSLNPQTEESQDPAPFLNRLVRRPSSAPKGRKTR 126

Qy 103 ARRAIAAHYVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYY 162

Db 127 ARRAIAAHYVHPRPGDGAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYY 186

Qy 163 LYCOVHFDEGKAVYIKLDLLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGS 222

Db 187 LYCOVHFDEGKAVYIKLDLLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGS 246

Qy 223 SLRIRTLPAWHLKAAPFLTYFGLFQVH 249

Db 247 SLRIRTLPAWHLKAAPFLTYFGLFQVH 273

RESULT 4

US-09-883-777-2

; Sequence 2, Application US/09883777

; Patent No. US20020110853A1

; GENERAL INFORMATION:

; APPLICANT: Wiley, Steven R.

; TITLE OF INVENTION: TWEAK RECEPTOR

; FILE REFERENCE: 2968-C

; CURRENT APPLICATION NUMBER: US/09/883,777

; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 60/203,347

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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:39:12 ; Search time 36 Seconds
(without alignments)
921.650 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARSQRRRRRRGGFTAL.....PWAHLKAAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

.l number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1268	100.0	249 20	AA09369 Human tumour necro
2	1268	100.0	249 21	AA07526 Amino acid sequenc
3	1268	100.0	249 21	AA07526 Human PRO207 antit
4	1268	100.0	249 23	AA086128 Human PRO207 polyp
5	1268	100.0	284 19	AA047525 Homo sapiens tumou
6	1268	99.8	249 19	AA047525 TNF related endoth
7	1265	99.8	249 22	AA000891 Human TREPA (TNF r
8	1066	84.1	273 22	AA003499 TWEAK extracellular
9	1062	83.8	208 20	AA093590 Human TNRL3 protei
10	1020	80.4	225 19	AA047524 Mus musculus tumou

11	1020	80.4	225 21	AA07527 Amino acid sequenc
12	968	76.3	211 20	AA093591 Mouse TNRL3 protei
13	792	62.5	189 19	AA029746 TNF related endoth
14	792	62.5	189 22	AA000892 Human UL4flag TREP
15	761	60.0	146 22	AA000895 Human TREPA (TNF r
16	116	9.1	325 22	AB067553 Drosophila melanog
17	116	9.1	409 23	AA077718 Drosophila melanog
18	108.5	8.6	211 21	AA058215 Canine mature CD15
19	108.5	8.6	260 21	AA058215 Canine CD154. Can
20	105.5	8.3	406 23	AA077717 Drosophila melanog
21	104	8.2	409 23	AA077716 Drosophila melanog
22	100	7.9	220 22	AA062340 Gp120 V3 loop-CD15
23	96	7.6	234 22	AA062339 Gp120 V3 loop-CD15
24	95.5	7.5	254 16	AA064190 Human 4-1BB-L poly
25	95.5	7.5	254 18	AA026657 Human 4-1BB ligand
26	95.5	7.5	254 23	AB075953 Human cytokine 4-1
27	94.5	7.5	240 23	AA013680 Human HVEM-binding
28	93.5	7.4	876 22	AB000217 Novel human diagno
29	93	7.3	1428 21	AA097033 Caspase 8-interact
30	92.5	7.3	208 20	AA031886 Human apoptosis in
31	92.5	7.3	208 20	AA06474 Human apoptosis in
32	92.5	7.3	208 21	AA018619 Partial human apop
33	92.5	7.3	208 23	AB081653 Human partial apop
34	92.5	7.3	240 23	AA013681 Human HVEM-binding
35	91.5	7.2	240 18	AA032255 Human apoptosis in
36	91.5	7.2	240 19	AA040362 Human Fas ligand-1
37	91.5	7.2	240 20	AA031885 Human apoptosis in
38	91.5	7.2	240 20	AA06473 Human apoptosis in
39	91.5	7.2	240 20	AA095033 Tumour necrosis fa
40	91.5	7.2	240 21	AA018618 A human apoptosis
41	91.5	7.2	240 21	AA078921 Human TL4. Homo s
42	91.5	7.2	240 22	AA048938 Human TL4 liver fu
43	91.5	7.2	240 23	AB081648 Human apoptosis in
44	91.5	7.2	240 23	AA013677 Human herpes virus
45	91.5	7.2	240 23	AA013679 Human HVEM-binding

ALIGNMENTS

RESULT 1
AA09369
ID AA09369 standard; Protein; 249 AA.
XX
AC AA09369;
AC
DT 15-JUL-1999 (first entry)
XX
DE Human tumour necrosis factor Apo-3 ligand protein sequence.
XX
KW Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis;
KW NF-kappaB-dependent transcription; JNK/SAPK-dependent response;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO9919490-A1.
XX
PD 22-APR-1999.
XX
PF 09-OCT-1998; 98WO-US21407.
XX
PR 17-DEC-1997; 97US-0069862.
PR 10-OCT-1997; 97US-0062037.
XX (GETH) GENENTECH INC.
PI Ashkenazi AJ, Marsters SA, Pitti R;
DR WPI: 1999-287982/24.
DR N-PSDB; AA056000.
XX
PT New human Apo-3 ligand (a tumour necrosis factor) homologue

XX PS Claim 1; Fig 1; 74pp; English.

XX CC The present sequence represents a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has CC cytostatic activity. Apo-3 ligand can be used to induce apoptosis in CC mammalian cancer cells, to induce NF-kappaB-dependent transcription and CC to induce JNK/SAPK-dependent responses in mammalian cells.

XX SQ Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 20; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-119; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0;

QY 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEEL 60
Db 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEEL 60

QY 61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120
61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120

QY 121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYKLD 180
Db 121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYKLD 180

QY 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240
Db 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240

QY 241 TYFGLFQVH 249
Db 241 TYFGLFQVH 249

RESULT 2
AAB07526
ID AAB07526 standard; protein; 249 AA.

AC AAB07526;
DT 20-OCT-2000 (first entry)

XX Amino acid sequence of a soluble recombinant human TWEAK protein.

XX TWEAK protein; immunological disorder; immune response; inflammation;
KW TWEAK blocking agent; autoimmune disease; organ transplant rejection;
KW Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour.

Homo sapiens.
WO200042073-A1.
20-JUL-2000.
14-JAN-2000; 2000WO-US01044.
15-JAN-1999; 99US-0116168.
(BIOJ) BIOGEN INC.
Rennett P;
WPI; 2000-476036/41.
Preventing and treating immune responses using modulators, especially
PT antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for
PT treating e.g. inflammation and graft versus host disease -
XX Disclosure; Fig 1; 45pp; English.
XX The present sequence represents a TWEAK protein. The specification

CC describes a method for preventing or treating an immunological
CC disorder and/or inhibiting an immune response in an animal. The
CC method comprises administering a TWEAK blocking agent. The method may
CC be used for preventing and treating immune disorders associated with
CC inappropriate expression and/or activity of TWEAK. These disorders
CC include autoimmune diseases, acute and chronic inflammation, organ
CC transplant rejection; Graft-versus-Host disease (GVHD), lymphoid cell
CC malignancies, septic and other forms of shock, loss of immune
CC responsiveness (as seen in human immunodeficiency virus (HIV)
CC infections) and failure of the immune response to tumour growth.

XX SQ Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 21; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-119; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0;

QY 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEEL 60
Db 1 MAARRSQRRRGRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEEL 60

QY 61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120
61 VAEEDQPSSELNPQTESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120

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Db 121 GAQAGVDGTVSGWEEARINSSPLRYNROI GEFIVTRAGLYLYLCVHFDEGKAVYKLD 180

QY 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240
Db 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRITLTPWAHLKAAPFL 240

QY 241 TYFGLFQVH 249
Db 241 TYFGLFQVH 249

RESULT 3
AAY95338
ID AAY95338 standard; protein; 249 AA.

AC AAY95338;
DT 25-SEP-2000 (first entry)

XX Human PRO207 antitumour protein.

XX PRO207; human; antitumour; tumour; therapy; cytostatic;
KW breast cancer; ovarian cancer; renal cancer; colorectal cancer;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer;
KW central nervous system cancer; melanoma; leukaemia; neoplasm.

Homo sapiens.
Key Location/Qualifiers
FT Key 1..40
FT Peptide /label= Signal_peptide
FT Protein 41..249
FT /label= PRO207
FT Modified-site 27..33 /note= "N-myristoylation"
FT Modified-site 29..35 /note= "N-myristoylation"
FT Modified-site 36..42 /note= "N-myristoylation"
FT Modified-site 45..51 /note= "N-myristoylation"
FT Modified-site 118..124 /note= "N-myristoylation"
FT Modified-site 121..127 /note= "N-myristoylation"
FT Modified-site 125..131

FT Modified-site /note= "N-myristoylation"
 FT 128..134
 FT Modified-site /note= "N-myristoylation"
 FT 139..143
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 10..14
 FT Modified-site /note= "amidation"
 FT 97..101
 FT Modified-site /note= "amidation"
 FT 24..35
 FT Peptide /note= "prokaryotic membrane lipoprotein lipid"
 FT
 XX WO200037638-A2.
 PN
 XX 29-JUN-2000.
 XX
 XX 02-DEC-1999; 99WO-US28565.
 XX
 XX 22-DEC-1998; 98US-0113296.
 XX 08-MAR-1999; 99WO-US05028.
 XX 21-APR-1999; 99US-0130232.
 XX 28-APR-1999; 99US-0131445.
 XX 14-MAY-1999; 99US-0134287.
 XX 20-JUL-1999; 99US-0144758.
 XX 26-JUL-1999; 99US-0145698.
 XX 15-SEP-1999; 99WO-US21090.
 XX 15-SEP-1999; 99WO-US21547.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
 PI Napier MA, Pitti RM, Wood WI;
 XX WPI: 2000-442668/38.
 DR N-PSDB; AAA49717.
 DR
 XX Novel composition to inhibit neoplastic cell growth or for treating
 PT tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,
 PT PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or
 PT PRO866 .
 XX
 XX Claim 19; Fig 4; 172pp; English.
 XX
 CC The present sequence is that of human antitumour protein PRO207,
 CC as deduced from a foetal kidney cDNA clone (see AAA49717). PRO207
 CC shows amino acid sequence identity to tumour necrosis factor family
 CC members, especially human lymphotxin-beta (23.4%) and human CD40
 CC ligand (19.8%). Mol.wt. is 27,216. A claimed method for inhibiting
 CC the growth of a tumour cell comprises exposing the tumor cell
 CC to PRO179, PRO207, PRO320, PRO221, PRO224, PRO328, PRO301,
 CC PRO526, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their
 CC agonists or chimeric polypeptides incorporating them. The tumour
 CC is especially a cancer selected from breast, ovarian, renal,
 CC colorectal, uterine, prostate, lung, bladder and central nervous
 CC system cancer, melanoma and leukaemia. Methods for the recombinant
 CC expression of the antitumour proteins are also provided.
 XX
 SQ Sequence 249 AA;
 Query Match 100.0%; Score 1268; DB 21; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.4e-119;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAARRSORRRGREGPTALLVPLALGLGLALACGLALLAWSLGSSASLSAQEPAQEL 60
 DB |||||
 DB 1 MAARRSORRRGREGPTALLVPLALGLGLALACGLALLAWSLGSSASLSAQEPAQEL 60
 QY 61 VAEDQDPSELNPQTESQDPAPFLNLVPRPSAPKGRKTRARRATAAHHVHPRGQD 120
 DB |||||
 DB 61 VAEDQDPSELNPQTESQDPAPFLNLVPRPSAPKGRKTRARRATAAHHVHPRGQD 120
 QY 121 GAQAGVDGTVSGWEEARINSSPLRNQIGEFIVTRAGLYLYYLCQVHDEGKAVYLKLD 180
 |||||

Db 121 GAQAGVDGTVSGWEEARINSSPLRNQIGEFIVTRAGLYLYYLCQVHDEGKAVYLKLD 180
 QY 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLTPWAHLKAAPFL 240
 |||||
 Db 181 LLVDGVLALRCLEEFSAATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLTPWAHLKAAPFL 240
 QY 241 TYFGLFQVH 249
 |||||
 Db 241 TYFGLFQVH 249
 |||||
 RESULT 4
 AAU86129
 ID AAU86129 standard; Protein; 249 AA.
 XX
 AC AAU86129;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human PRO207 polypeptide.
 XX
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoeleic disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW cytostatic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200153486-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 11-FEB-2000; 2000WO-US03565.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 11-MAR-1999; 99US-123972P.
 PR 11-MAY-1999; 99US-133459P.
 PR 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-140650P.
 PR 22-JUN-1999; 99US-140653P.
 PR 20-JUL-1999; 99US-144758P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 17-AUG-1999; 99US-149395P.
 PR 31-AUG-1999; 99US-151689P.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
 PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX
 XX WPI: 2002-205567/26.
 DR N-PSDB; ABK40255.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for
 PT treating benign or malignant tumours, leukaemias and lymphoid
 PT malignancies, inflammatory, angiogenic and immunologic disorders -
 XX
 PS Claim 61; Fig 4; 302pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,
 CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
 CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,

CC macrophagal, stromal and blastocoelic disorders, inflammatory, immune
 CC and angiogenic disorders. The polynucleotide sequences are also
 CC useful in gene therapy. AAU86128-AAU86162 represent the human PRO
 CC polypeptides of the invention.

XX SQ Sequence 249 AA;

Query Match 100.0%; Score 1268; DB 23; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.4e-119;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARRSORRRGRGEGPTALLVPLALGLALACLGILLAVVSLGSRASLSAQEPQAEEL 60
 Db 1 MAARRSORRRGRGEGPTALLVPLALGLALACLGILLAVVSLGSRASLSAQEPQAEEL 60

Qy 61 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 120
 Db 61 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 120

Qy 121 GAAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHFDGKAVYKLD 180
 121 GAAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHFDGKAVYKLD 180

Qy 181 LLVDGVLAALRCLEEFSAATAASSLGQPLRCQVSGLLALRPQSSLRIRTLPAHLKAAPFL 240
 Db 181 LLVDGVLAALRCLEEFSAATAASSLGQPLRCQVSGLLALRPQSSLRIRTLPAHLKAAPFL 240

Qy 241 TYFGLFQVH 249

Db 241 TYFGLFQVH 249

RESULT 5

ID AAW47525 standard; *Protein; 284 AA.

AC AAW47525;

DT 21-JUL-1998 (first entry)

XX Homo sapiens tumour necrosis factor related ligand (TREL).

XX TREL; tumour necrosis factor related ligand; tnfr, treatment;
 KW cancer; autoimmune disease; immune system; stimulation; suppression;
 KW graft rejection.

OS Homo sapiens.

XX WO9805783-A1.

XX 12-FEB-1998.

XX 07-AUG-1997; 97WO-US13945.

XX 18-MAR-1997; 97US-0040820.

XX 07-AUG-1996; 96US-0023541.

XX 18-OCT-1996; 96US-0028515.

XX (BIOJ) BIOGEN INC.
 XX (UYGE-) UNIV GENEVA FACULTY MEDICINE.

XX Browning JL, Chicheportiche Y;

XX WPI; 1998-145619/13.

XX N-PSDB; AAV18600.

XX Tumour necrosis factor related ligand - useful for, e.g. treating
 PT cancer, auto-immune disease and immune responses to tissue grafts

XX Claim 12; Pages 50-51; 69pp; English.

XX The sequence is that of human tumour necrosis factor related
 CC ligand (TREL). TREL or active fragments can be included with a

CC carrier in pharmaceutical compositions to treat cancer, autoimmune
 CC diseases or immune responses to tissue grafts, or to stimulate or
 CC suppress the immune system. It is useful to screen for TREL
 CC receptors, by labelling with a detectable label and screening
 CC compositions for binding. Agents interfering with TREL-receptor
 CC binding can also be screened for, can then be administered,
 CC optionally with interferon- gamma, to induce cell death or
 CC treat, suppress or alter immune responses (especially involving human
 CC adenocarcinoma cells) involving a signal pathway between TREL and its
 CC receptor. It's coding sequence can be used in gene therapy for
 CC TREL-related disorders in mammals (especially humans), e.g. tumours,
 CC autoimmune and inflammatory diseases or inherited genetic disorders,
 CC by introducing into cells, and expressing, therapeutically effective
 CC amounts of a vector, e.g. a virus comprising a gene encoding TREL.
 CC It may also be of use in the preparation of probe probes for
 CC screening natural/synthetic DNAs for TREL-encoding sequences
 CC and for antisense therapy.

XX SQ Sequence 284 AA;

Query Match 100.0%; Score 1268; DB 19; Length 284;
 Best Local Similarity 100.0%; Pred. No. 1.7e-119;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARRSORRRGRGEGPTALLVPLALGLALACLGILLAVVSLGSRASLSAQEPQAEEL 60

Db 36 MAARRSORRRGRGEGPTALLVPLALGLALACLGILLAVVSLGSRASLSAQEPQAEEL 95

Qy 61 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 120

Db 96 VAEDQDPSELNPQTEESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGQD 155

Qy 121 GAAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHFDGKAVYKLD 180

Db 156 GAAQAGVDGTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCQVHFDGKAVYKLD 215

Qy 181 LLVDGVLAALRCLEEFSAATAASSLGQPLRCQVSGLLALRPQSSLRIRTLPAHLKAAPFL 240

Db 216 LLVDGVLAALRCLEEFSAATAASSLGQPLRCQVSGLLALRPQSSLRIRTLPAHLKAAPFL 275

Qy 241 TYFGLFQVH 249

Db 276 TYFGLFQVH 284

RESULT 6

AAW29745

ID AAW29745 standard; Protein; 249 AA.

XX AAW29745;

XX 27-OCT-1998 (first entry)

XX TNF related endothelium proliferative agent protein.

XX TNF; endothelium proliferative agent; TRPA; wound healing; cancer;
 KW tissue grafting; vascularisation; apoptosis; autoimmune; birth control.

XX Homo sapiens.

XX WO9835061-A2.

XX 13-AUG-1998.

XX 12-FEB-1998; 98WO-US02859.

XX 10-FEB-1998; 98US-0021706.

XX 12-FEB-1997; 97US-0798692.

XX (ABBO) ABBOTT LAB.

XX Wiley SR;

DR WPI: 1998-447255/38.
 DR N-PSDB; AAV47613.
 XX Detecting nucleic acid encoding TREPA - useful for diagnosis and
 PT treatment of autoimmune disease, tumours and inflammation
 XX
 PS Claim 16; Page 123-4; 142pp; English.
 XX
 CC The TNF-related endothelium proliferative agent (TREPA), or its
 CC activators or agonists, are used to treat a deficit of TREPA, e.g. to
 CC promote wound healing or tissue grafting, by promoting vascularisation,
 CC also to induce apoptosis for treating cancer and eliminating autoreactive
 CC T cells, as an adjunct to cancer chemotherapy or antiviral treatment.
 CC TREPA peptides can also be used to target cytotoxic agents or for
 CC affinity isolation of the corresponding receptor, the nucleic acid for
 CC which can be used to transform tumour cells to render them more
 CC responsive to TREPA and to screen for TREPA mimics.
 CC Ribozymes, antisense RNA, antibodies or peptides, are used to treat
 CC TREPA-associated diseases, e.g. tumours and metastases (by inhibiting
 CC vascularisation), inflammation or a wide range of autoimmune conditions,
 CC conditions involving abnormal stimulation of epithelial cells (e.g.
 CC atherosclerosis), for birth control (inhibiting ovulation and placental
 CC formation) or other angiogenic conditions (e.g. ulcers).
 XX
 CC Sequence 249 AA;
 Query Match 99.8%; Score 1265; DB 19; Length 249;
 Best Local Similarity 99.6%; Pred. No. 2.8e-119;
 Matches 248; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLLLAVVSLGSRASLSAQEPAGEEL 60
 Db 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLLLAVVSLGSRASLSAQEPAGEEL 60
 QY 61 VAEDDQPSSELPNPTESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHVEVHPRGQD 120
 Db 61 VAEDDQPSSELPNPTESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHVEVHPRGQD 120
 QY 121 GAQAGVDGTVSGWEARINSSEPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180
 Db 121 GAQAGVDGTVSGWEARINSSEPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180
 QY 181 LLVDGVIALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240
 Db 181 LLVDGVIALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240
 QY 241 TYFGLFQVH 249
 Db 241 TYFGLFQVH 249
 RESULT 7
 AAE00891
 ID AAE00891 standard; Protein; 249 AA.
 XX
 AC AAE00891;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human TREPA (TNF related endothelium proliferative agent).
 XX
 KW Human; tumour necrosis factor; TNF; angiogenesis; wound healing;
 KW TREPA; TNF related endothelium proliferative agent; tumour; metastasis;
 KW grafting; relnary.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 98..249
 FT /label= Extracellular_domain
 FT
 PN US6207642-B1.
 XX

PD 27-MAR-2001.
 XX
 PF 26-JUN-1998; 98US-0105343.
 XX
 PR 12-FEB-1997; 97US-0798692.
 PR 10-FEB-1998; 98US-0021706.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Wiley SR;
 XX
 DR WPI; 2001-280760/29.
 DR N-PSDB; AAD04350.
 XX
 PT Inducing angiogenesis in mammal at desired sites for promoting wound
 PT healing, by administering soluble fragment of extracellular domain of
 PT tumor necrosis factor related endothelium proliferative agent protein
 PT
 PS Claim 1; Column 75-76; 53pp; English.
 XX
 CC The present invention relates to extracellular signal molecules,
 CC particularly members of tumour necrosis factor (TNF) family molecules
 CC designated as TREPA (TNF related endothelium proliferative agent).
 CC Soluble biologically active TREPA are used to treat TREPA-associated
 CC diseases, tumours or metastases. TREPA is used for inducing angiogenesis
 CC in human for promoting wound healing and for vascularising grafted
 CC tissue for successful grafting and to promote tissue grafts.
 CC The present amino acid sequence is clone ID #690050 human TREPA..
 XX
 CC Sequence 249 AA;
 Query Match 99.8%; Score 1265; DB 22; Length 249;
 Best Local Similarity 99.6%; Pred. No. 2.8e-119;
 Matches 248; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLLLAVVSLGSRASLSAQEPAGEEL 60
 Db 1 MAARRSRRRRGEGPTALLVPLALGLGLALACGLLLAVVSLGSRASLSAQEPAGEEL 60
 QY 61 VAEDDQPSSELPNPTESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHVEVHPRGQD 120
 Db 61 VAEDDQPSSELPNPTESQDPAPFLNRLVRRPSAPKGRKTRARRAIAAHVEVHPRGQD 120
 QY 121 GAQAGVDGTVSGWEARINSSEPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180
 Db 121 GAQAGVDGTVSGWEARINSSEPLRYNRQIGEFIVTRAGLYLYLYCQVHFDGKAVYLKLD 180
 QY 181 LLVDGVIALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240
 Db 181 LLVDGVIALRCLEEFSAATAASSLGQRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFL 240
 QY 241 TYFGLFQVH 249
 Db 241 TYFGLFQVH 249
 RESULT 8
 AAU03499
 ID AAU03499 standard; Protein; 273 AA.
 XX
 AC AAU03499;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE TWEAK extracellular domain-containing fusion protein.
 XX
 KW TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis;
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;
 KW rubecosis; uveitis; macular degeneration; arthritis; rheumatism;
 KW corneal graft neovascularisation; psoriasis; metastatic condition;
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
 KW

KW preneoplastic condition; myocardial angiogenesis; wound granulation;
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;
 KW peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
 KW fusion protein.

XX Homo sapiens.
 OS Synthetic.

XX WO200145730-A2.

PN 28-JUN-2001.

XX 19-DEC-2000; 2000WO-US34755.

XX 20-DEC-1999; 99US-0172878.

PR 10-MAY-2000; 2000US-0203347.

XX (IMMUNEX CORP.

PA Wiley SR;

XX WPI; 2001-417975/44.

DR N-PSDB; AAS03964.

XX Modulating angiogenesis in a mammal for treating diseases mediated by
 PT angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or
 PT peripheral tissue, by administering antagonist or agonist of TWEAK
 PT receptor -

PS Example 1; Page 41; 46pp; English.

XX The sequence represents a fusion protein encoded by the
 CC expression vector pDC409-LZ-TWEAK. The fusion protein comprises a
 CC growth hormone leader, a leucine zipper multimerisation domain, and
 CC the extracellular domain of human TWEAK. The fusion protein was
 CC used in the isolation of human TWEAK receptor (TWEAKR)-expressing
 CC clones from a COS cell human cDNA library. The TWEAK protein is
 CC a member of the tumour necrosis factor (TNF) family and induces
 CC angiogenesis. TWEAKR may therefore be used to screen for and
 CC develop TWEAKR agonists and antagonists for the modulation of
 CC angiogenesis, to be used in the treatment and diagnosis of human disease.
 CC The disorders mediated by angiogenesis include ocular disorders
 CC characterised by ocular neovascularisation such as diabetic retinopathy,
 CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity,
 CC retrolental fibroplasia, rubecosis, uveitis, macular degeneration and
 CC corneal graft neovascularisation, and inflammatory diseases such as
 CC arthritis, rheumatism and psoriasis. Other treatable diseases include
 CC malignant and metastatic conditions such as sarcomas and carcinomas,
 CC benign tumours and preneoplastic conditions, myocardial angiogenesis,
 CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
 CC plaque neovascularisation, telangiectasia, wound granulation, coronary
 CC atherosclerosis, peripheral atherosclerosis and ischaemia.

XX Sequence 273 AA;

Query Match 84.1%; Score 1066; DB 22; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4e-99;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SLGSRASLSAQEPQAEELVAEEDQDPSELNQTESQDPAPFLNLRVPRRSAPKGRKTR 102

DB 67 SLGSRASLSAQEPQAEELVAEEDQDPSELNQTESQDPAPFLNLRVPRRSAPKGRKTR 126

QY 103 ARRAIAHYEHPRPQDGAQVGDGTSGWEEARINSSPLRYNRQIGEIFVTRAGLYY 162

DB 127 ARRAIAHYEHPRPQDGAQVGDGTSGWEEARINSSPLRYNRQIGEIFVTRAGLYY 186

QY 163 LYCQVHFDEGKAVYKLDLLVDGVLALRCLEEFNSATAASSLGPQLRCQVSGLLALRPGS 222

DB 167 LYCQVHFDEGKAVYKLDLLVDGVLALRCLEEFNSATAASSLGPQLRCQVSGLLALRPGS 246

QY 223 SLRIRTLPAHLKAAFFLYTYGLFQVH 249

DB 247 SLRIRTLPAHLKAAFFLYTYGLFQVH 273

RESULT 9

AAW93590

ID AAW93590 standard; Protein; 208 AA.

XX AAW93590;

AC AAW93590;

XX 18-JUN-1999 (first entry)

DT Human TNRL3 protein.

XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;

KW developmental abnormality; gestational abnormality; prostate cancer;

KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;

KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;

KW apoptosis; human.

XX Homo sapiens.

XX WO9911791-A2.

PN 11-MAR-1999.

PD 04-SEP-1998; 98WO-US18393.

XX 05-SEP-1997; 97US-0924634.

PR (UNIW) UNIV WASHINGTON.

XX Chaudhary PM;

XX WPI; 1999-205191/17.

DR N-PSDB; AAX23424.

XX New Tumor Necrosis Factor family receptor polypeptides and ligands -

PT useful for diagnosis and treatment of prostate cancer and

PT developmental or gestational abnormalities

XX Claim 40; Fig 13A; 156pp; English.

XX This invention describes isolated Tumor Necrosis Factor (TNF) family

CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active

CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or

CC their active fragments. APO4 is useful for diagnosing prostate cancer

CC by determining levels of APO4 in an individual. Prostate cancer can also

CC be treated using APO4 selective binding agents linked to a therapeutic

CC moiety. APO4 polypeptides are also useful for identifying selective

CC binding agents, useful in diagnosis/treatment of disease by binding of

CC agents to the polypeptide/active fragment which is extracellular. Or

CC vivo. APO4 polypeptides/ active fragments are also useful for screening

CC for agonists and antagonists by binding and observing the change in APO4

CC activity. Effective pharmacological agents useful in diagnosis or

CC treatment of disease are also identified using APO4 polypeptides/active

CC fragments and APO4 signal transducer molecules that specifically interact

CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4

CC activity. The method is performed in vivo or in vitro. APO polypeptides

CC are all useful as immunogens for preparing antibodies. APO4 is also

CC useful for diagnosis/treatment of developmental or gestational

CC abnormalities. APO8 was transfected to human breast carcinoma cell line

CC MCF-7, and induced apoptosis.

XX Sequence 208 AA;

QY Query Match 83.8%; Score 1062; DB 20; Length 208;

Best Local Similarity 99.5%; Pred. No. 6.8e-99;

Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 42 VSLGSRASLSAQEPQAEELVAEEDQDPSELNQTESQDPAPFLNLRVPRRSAPKGRKT 101

Db 1 VLSGRASLSAQEAQELVAEDDPSSELNPQTEESQDPAPFLNRLVPRRSAPKGRKT 60
 QY 102 RARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEARINSSSPLRYNRQIGEFIVTRAGLY 161
 Db 61 RARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEARINSSSPLRYNRQIGEFIVTRAGLY 120
 QY 162 YLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLPQLRCQVSGLLALRPG 221
 Db 121 YLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLPQLRCQVSGLLALRPG 180
 QY 222 SSLRIRTLPAWHLKAAPLTYFGLFOVH 249
 Db 181 SSLRIRTLPAWHLKAAPLTYFGLFOVH 208
 RESULT 10
 AAW47524
 ID AAW47524 standard; Protein; 225 AA.
 YV AAW47524;
 L. 21-JUL-1998 (first entry)
 XX Mus musculus tumour necrosis factor related ligand (TRELL).
 DE TRELL; tumour necrosis factor related ligand; tnfr; treatment;
 KW cancer; autoimmune disease; immune system; stimulation; suppression;
 KW graft rejection.
 KW
 XX Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..21
 FT /note= "hydrophobic, transmembrane domain"
 XX
 PN WO9805783-A1.
 XX 12-FEB-1998.
 PD
 PF 07-AUG-1997; 97WO-US13945.
 XX
 XX 18-MAR-1997; 97US-0040820.
 PR 07-AUG-1996; 96US-0023541.
 PR 18-OCT-1996; 96US-0028515.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (UYGE-) UNIV GENEVA FACULTY MEDICINE.
 PA
 AAW
 DR Browning JL, Chicheportiche Y;
 DR WPI; 1998-145619/13.
 XX N-PSDB; AAV18599.
 XX
 PT Tumour necrosis factor related ligand - useful for, e.g. treating
 PT cancer, auto-immune disease and immune responses to tissue grafts
 XX
 PS Claim 12; Pages 48-50; 69pp; English.
 XX
 CC The sequence is that of mouse tumour necrosis factor related
 CC ligand (TRELL). TRELL or active fragments can be included with a
 CC carrier in pharmaceutical compositions to treat cancer, autoimmune
 CC diseases or immune responses to tissue grafts, or to stimulate or
 CC suppress the immune system. It is useful to screen for TRELL
 CC receptors, by labelling with a detectable label and screening
 CC compositions for binding. Agents interfering with TRELL-receptor
 CC binding can also be screened for, can then be administered,
 CC optionally with interferon- gamma, to induce cell death or
 CC treat, suppress or alter immune responses (especially involving human
 CC adenocarcinoma cells) involving a signal pathway between TRELL and its
 CC receptor. It's coding sequence can be used in gene therapy for
 CC TRELL-related disorders in mammals (especially humans), e.g. tumours,
 CC autoimmune and inflammatory diseases or inherited genetic disorders,
 CC by introducing into cells, and expressing, therapeutically effective

CC amounts of a vector, e.g. a virus comprising a gene encoding TRELL.
 CC It may also be of use in the preparation of prepare probes for
 CC screening natural/synthetic DNAs for TRELL-encoding sequences
 CC and for antisense therapy.
 XX
 SQ Sequence 225 AA;
 Query Match 80.4%; Score 1020; DB 19; Length 225;
 Best Local Similarity 88.8%; Pred. No. 1.3e-94;
 Matches 199; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 26 LSLGLALACLGILLAVVSLGSRASLSAQEAQELVAEDDPSSELNPQTEESQDPAPFL 85
 Db 2 LSLGLALACLGILLAVVSVLSGWSATLSAQEPSQBELTADRRPELNPQTEESQDVVFFL 61
 QY 86 NLRVPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEARINSSSPLR 145
 Db 62 EQLVPRRSAPKGRKTRARRAIAAHYEVHPRPGDGAQAGVDGTVSGWEATKINSSPLR 121
 QY 146 YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYKLDLLVDGVLALRCLEEPSATASLSGLP 205
 Db 122 YDRQIGEFIVTRAGLYYLYCQVHFDEGKAVYKLDLLVNGVLALRCLEEPSATASSPGP 181
 QY 206 QLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPLTYFGLFOVH 249
 Db 182 QLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPLTYFGLFOVH 225
 RESULT 11
 AAB07527
 ID AAB07527 standard; protein; 225 AA.
 AC AAB07527;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of a soluble recombinant murine TWEAK protein.
 XX TWEAK protein; immunological disorder; immune response; inflammation;
 KW TWEAK blocking agent; autoimmune disease; organ transplant rejection;
 KW Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour.
 XX
 OS Mus sp.
 XX WO2000042073-A1.
 PN
 XX 20-JUL-2000.
 PD
 XX 14-JAN-2000; 2000WO-US01044.
 PF
 XX 15-JAN-1999; 99US-0116168.
 PR
 XX (BIOJ) BIOGEN INC.
 PA
 XX Rennert P;
 PI
 XX WPI; 2000-476036/41.
 DR
 XX Preventing and treating immune responses using modulators, especially
 PT antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for
 PT treating e.g. inflammation and graft versus host disease -
 PS Disclosure; Fig 1; 45pp; English.
 XX
 CC The present sequence represents a TWEAK protein. The specification
 CC describes a method for preventing or treating an immunological
 CC disorder and/or inhibiting an immune response in an animal. The
 CC method comprises administering a TWEAK blocking agent. The method may
 CC be used for preventing and treating immune disorders associated with
 CC inappropriate expression and/or activity of TWEAK. These disorders
 CC include autoimmune diseases, acute and chronic inflammation, organ
 CC transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell
 CC malignancies, septic and other forms of shock, loss of immune

This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic moiety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of

xx Detecting nucleic acid encoding TREPA - useful for diagnosis and
PT treatment of autoimmune disease, tumours and inflammation
XX
XX
PS Claim 16; Page 125-6; 142pp: English.
XX
CC The TNF-related endothelium proliferative agent (TREPA), or its

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:14 ; Search time 14 Seconds
(without alignments)
523.308 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268
Sequence: 1 MAARRSQRGRGEGFTAL.....PWAHLKAAPFLYGLFQVH 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

rchred: 262574 seqs, 29422922 residues

al number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: +
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1265	99.8	249	4	US-09-105-343A-2
2	792	62.5	189	4	US-09-105-343A-3
3	761	60.0	146	4	US-09-105-343A-6
4	95.5	7.5	254	1	US-08-236-918A-4
5	95.5	7.5	254	4	US-09-150-864A-4
6	91.5	7.2	240	4	US-08-913-014A-1
7	91.5	7.2	240	4	US-09-072-993C-4
8	90	7.1	659	4	US-09-562-737-11
9	90	7.1	660	3	US-08-819-177-1
10	89	7.0	256	4	US-09-320-424-13
11	88.5	7.0	659	4	US-09-562-737-18
12	87	6.9	253	4	US-09-320-424-11
13	87	6.9	253	4	US-08-670-354-6
14	87	6.9	231	1	US-09-320-424-6
15	87	6.9	231	5	PCT-US96-10895-6
16	86	6.8	1323	1	US-08-026-138E-4
17	85	6.7	294	3	US-08-996-139-11
18	85	6.7	294	4	US-08-995-659-11
19	85	6.7	294	4	US-09-215-649A-11
20	85	6.7	294	4	US-09-577-780-11
21	83.5	6.6	247	4	US-09-157-864-4
22	83.5	6.6	885	1	US-08-042-747A-8
23	83.5	6.6	885	3	US-08-804-439A-23
24	83.5	6.6	885	3	US-08-720-229-23
25	82	6.5	248	3	US-08-341-018-52
26	82	6.5	248	4	US-08-470-335-210
27	82	6.5	248	4	US-08-470-339-210

28	82	6.5	248	4	US-08-467-602-207	Sequence 207, App
29	82	6.5	248	4	US-08-467-602-404	Sequence 404, App
30	82	6.5	349	4	US-08-470-335-188	Sequence 188, App
31	82	6.5	382	4	US-08-467-602-382	Sequence 382, App
32	82	6.5	405	4	US-08-467-602-384	Sequence 384, App
33	82	6.5	411	4	US-08-470-339-189	Sequence 189, App
34	82	6.5	414	4	US-08-470-339-188	Sequence 188, App
35	82	6.5	422	1	US-08-036-555B-170	Sequence 170, App
36	82	6.5	422	1	US-08-469-569-170	Sequence 170, App
37	82	6.5	422	1	US-08-428-926-3	Sequence 170, App
38	82	6.5	422	1	US-08-249-322A-170	Sequence 170, App
39	82	6.5	422	1	US-08-428-927-3	Sequence 3, Appli
40	82	6.5	422	1	US-08-428-298-3	Sequence 3, Appli
41	82	6.5	422	1	US-08-339-517-3	Sequence 3, Appli
42	82	6.5	422	1	US-08-469-526A-170	Sequence 170, App
43	82	6.5	422	2	US-08-734-591A-170	Sequence 170, App
44	82	6.5	422	2	US-08-469-660-170	Sequence 170, App
45	82	6.5	422	3	US-08-341-018-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-09-105-343A-2
; Sequence 2, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S. R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09105.343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
; US-09-105-343A-2

Query Match 99.8%; Score 1265; DB 4; Length 249;
Best Local Similarity 99.6%; Pred. No. 4.3e-120;
Matches 248; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAARRSQRGRGEGFTALVPLALGLALACLLGLLAVSLGSRASLSAQEPQAEEL 60

Db 1 MAARSRKRRGREGPTALLVPLALGLGLALACLLGLLLAVSLGSRASLSAQEPAGEEL 60
QY 61 VAEDQDPSELNPQTEESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120
Db 61 VAEDQDPSELNPQTEESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120
QY 121 GAQAGVDGTVSGWEAEARINSSPLRYNRQIGFEFIVTRAGLYLYLCQVHDEGKAVYKLD 180
Db 121 GAQAGVDGTVSGWEAEARINSSPLRYNRQIGFEFIVTRAGLYLYLCQVHDEGKAVYKLD 180
QY 181 LLDVGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPGLSSLRIRITLPAWHLKAAPFL 240
Db 181 LLDVGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPGLSSLRIRITLPAWHLKAAPFL 240
QY 241 TYFGLFQVH 249
Db 241 TYFGLFQVH 249
RESULT 2
US-09-105-343A-3
; Sequence 3, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-3
Query Match 62.5%; Score 792; DB 4; Length 189;
Best Local Similarity 99.3%; Pred. No. 1.9e-72;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 97 KGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEAEARINSSPLRYNRQIGFEFIVT 156
Db 37 KGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEAEARINSSPLRYNRQIGFEFIVT 96

QY 157 RAGLYLYLCQVHDEGKAVYKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLL 216
Db 97 RAGLYLYLCQVHDEGKAVYKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLL 156
QY 217 ALRPGSSLRIRITLPAWHLKAAPFLTYFGLFQVH 249
Db 157 ALRPGSSLRIRITLPAWHLKAAPFLTYFGLFQVH 189
RESULT 3
US-09-105-343A-6
; Sequence 6, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-6
Query Match 60.0%; Score 761; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.8e-69;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEAEARINSSPLRYNRQIGFEFIVTRAGLYYL 163
Db 1 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEAEARINSSPLRYNRQIGFEFIVTRAGLYYL 60
QY 164 YCQVHDEGKAVYKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPSS 223
Db 61 YCQVHDEGKAVYKLDLLVDGVLLALRCLEFSATASSLGQPLRLCOVSGLLALRPSS 120
QY 224 LRIRITLPAWHLKAAPFLTYFGLFQVH 249
Db 121 LRIRITLPAWHLKAAPFLTYFGLFQVH 146
RESULT 4
US-08-236-918A-4

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Query Match          7.5%; Score 95.5; DB 1; Length 254;
Best Local Similarity 25.7%; Pred. No. 0.075;
Matches 66; Conservative 31; Mismatches 87; Indels 73; Gaps 11;

19 ALLVPLAIGLGLACLGLLLAVSL--GSRASL--SAQEPAQEELVAEDQDPSELNPQTE 76
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
30 ALVAGLLULLLLAAACAVFLACPWAVSGARASPGSAASPLRE-----GPGLSP--- 78
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
77 ESODPAPFLNRLVRPRSPAKPKRKTARRAIAAHYEVHPRPGDGAQAGVDGTSGWEE- 135
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
79 --DDPAGLLDL-----RGMAFALVAQNVL-----IDGPLSWYSDP 113
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
136 --ARINSSPLRYNRQICEFIVTRAGLYLYLCQVHFDEGKAVYLLKLDLLVDG-----VL 187
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
114 GLAGVSLTGGLSYKEDTKELVAKAGVYVFFQ-----LELRVAVAGEGSGVSL 163
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188 ALRCLEEFSTAASSLGQRLCQVSG-----LLALPGSSLRTRTUPWAHLK 235
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
164 ALHLQPLRSAAGAALALTVDLPASSEARNSAFGQGRLLHLHGAGQLRGVLLHTEARAR 223
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236 AAPFL-----TYFGLFOV 248
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224 HAWQLTGATVLGLFRV 240
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RESULT 5
US-09-150-864A-4
; Sequence 4, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:

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/ COUNTRY: USA
/
/ ZIP: 02109
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/ COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Diskette
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/ COMPUTER: IBM Compatible
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/ OPERATING SYSTEM: DOS
/
/ SOFTWARE: FastSeq for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/913,014A
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/ FILING DATE: 04-SEP-1997
/
/ CLASSIFICATION: 424
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: PCT/JP97/02480
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QY 121 GAQAGVDTGSGWEARINSSPLRYNRGIEFIVTRAGLYLYYCQVHF 169
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Db 118 NEKA-LGRKINSWESSRGSHSFLSNLHLRNGELVHIEKGFYIYSQTF 165

RESULT 11
US-09-562-737-18
; Sequence 18, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synt
; OTHER INFORMATION: Sequence
; OTHER INFORMATION:
US-09-562-737-18

      Query Match          7.0%; Score 88.5; DB 4; Length 659
      Best Local Similarity 24.4%; Pred. No. 1.4;
      Matches 38; Conservative 18; Mismatches 57; Indels

QY 18 TALLVPLALGLALACLGILLAVVLSGRASLSAQPRAQELVA-----
Db 64 TLSLIPPRAG-----LUSAKSSGAGSRLLAEMQLMDLIMAAAGDTPGCA
QY 68 PSELN-----POTESQDPAPFLNLRVRRRSAPKGRKT-----RARRA
Db 114 DDELQAQPGVGVPRAESNQDPA-----SSOGQPGTGTGYRPKPKE
QY 114 HPRPQDGAQAGVDGTGVSWEARINSSSPLRYNRQ 149
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 QVPWSQDTLNNNSYGGKHSWQDRASRSSPLKTDQ 200

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

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Db 144 -ISKDGTKLG--QKIESWESSRGKHSFLNHLVFRNGELVIEQGLYYIISQTYF 194
RESULT 14
US-09-320-424-6
; Sequence 6, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 291
; TYPE: PRT
; ORGANISM: murine
; US-09-320-424-6

Query Match 6.9%; Score 87; DB 4; Length 291;
Best Local Similarity 27.2%; Pred. No. 0.65;
Matches 31; Conservative 16; Mismatches 53; Indels 14;

QY 58 EELVAEDQDPSELNPOTESQDPAPFLNLVPRRSAP--KGRKTRARRAIAAHYEV
Db 93 EEVTLRTFQDTISTVPEKQLSTPLP---RGRPKQKVAAHITGITRRNSALIP-----
QY 116 RPOGDGAQAQVDGTVSGWEARINSSPLRYNQIGEFIVTRAGLYLYCOVHF 169
Db 144 -ISKDGTKLG--QKIESWESSRGKHSFLNHLVFRNGELVIEQGLYYIISQTYF 194

RESULT 15
PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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```

; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10895-6

      very Match          6.9%; Score 87; DB 5; Length 291;
      1st Local Similarity 27.2%; Pred. No. 0.65;
      Matches 31; Conservative 16; Mismatches 53; Indels 14; Gaps 4;

Qy 58 BELVAEEQDPSELNPQTEESQDPAPFLNRLVPRRSAP--KGRKTRARRAIAAHYEVHP 115
Db 93 EEVLTURTFODTISTVPEKQLSTPPLP---RGGRPQKVAAHITGTRRSNSALIP----- 143
Qy 116 RPDGAGAGVDGTGSGWEARINSSPLRYNQIGEFIVTRAGLYLYLCQVHF 169
Db 144 -ISKDKTLG--QKIESWESSRKHSFLNHVLFNGELVIEQEGLYIYSQTYF 194
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Search completed: April 12, 2003, 08:39:40
Job time : 16 secs

Query/March 7.3%; Score 93; DB 2; Length 378;
Best Local Similarity 25.6%; Pred. No. 3;
Matches 68; Conservative 28; Mismatches 98; Indels 72; Gaps 12;

QY 9 RRRRR--GEPQTALLVPLALGLGALACLGALLAVSLGSRASLSAQEPA--QEELVAE 63
DB 50 REGDVRVVGQFIATLTLSALEGGDSFAVLSR-----SLGROSSAAGSRAAATQAA LAE 104
QY 64 EDQDPSELNPQTESQDPAPFLNRLVRPRRS--APGGRKTRAR-----RAIAAHYEVHP 115
DB 105 SRQ-----LTORRAALNRELAERKSLALQTERLTLLAREAVARAETIAAGQPLSP 154
QY 116 RPDGCAQAGVDCTVSGHEEARINSSPLRYNRQIGFIVTRAGLYLYLCVQHFDEGKAV 175
DB 155 RE----LOARRSAELAVQOEASTLSSQALSRYERQIGEV-----DARLA 193
QY 176 YLKLDL---LVDGVLALRCLEFSATAASSLGPQLRLCQVSGLLA----- 217
DB 194 AIPDLOARAENASTLAGLEQ-QATQVEAQGRYVVATVAGRVAAALPVEAGQTVGVGAA 252
218 ---LRPGSLRLRITLPWAHLKAAPFL 240
DB 253 VAVLTGDSALVAEL-YAPSRAGFV 277

RESULT 6
A70611
hypothetical protein Rvi219c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: A70611
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70611
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-212 <COL>
A:Cross-references: GB:293777; GB:AL123456; NID:g3261726; PID:CAB07841.1; PID:e1299832
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rvi219c

Query Match	7.2%	Score 91.5;	DB 2;	Length 212;
Best Local Similarity	24.5%;	Pred. No. 2.1;		
Matches 53;	Conservative 26;	Mismatches 78;	Indels 59;	Gaps 9;
QY	11	GRRCPTGALLVPLALGLGL-----ALACLGILLAVSLGSRASLSAQEPAOEELVAEE--	64	
DB	21	GRHG-----FGVGLRAIAEAGVSAALVIHHFGSKEGL---RKACDDFFVAEIR	66	
QY	65	-----DQPSLNPGTESQDPAPFLNLVLRPRSPAPKGRKTRARRAJAHYEVHPR	116	
DB	67	SSKAALKSNDPTTTLAQMAIESYAPLMAYLVRSMOSGGELAKMLWKMI-----	117	
QY	117	PGQDGAQGVDTGVTSGWEEARINSSPLRYNQRIGEFI-VTRAGLYLYLCOVHFD----	170	
DB	118	-----DNAREYLD-----EGVRAGTVKSRDPRARFLAITGGGGFLYLQMHENPTDLR	168	
QY	171	-----EGKAVYLKDLLVDGVLAIRCL--EFSATA	199	
DB	169	AALRDYAHDMVLPSEVYVTEGLLADRAMYEAFLEAE	204	

RESULT 7
S41710
mitosis-specific cyclin 2 - garden snapdragon
C;Species: *Antirrhinum majus* (garden snapdragon)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 16-Jul-1999

[illegible]

Db 189 HLLSPSSVFFGAF 202

RESULT 12

D70745
 hypothetical protein rv0497 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: D70745
 R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: D70745
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 Residues: 1-310 <COL>
 Cross-references: GB:277162; GB:AL123456; NID:g3261606; PIDN:CAB00923.1; PID:e255036;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv0497

Query Match 6.9%; Score 87; DB 2; Length 310;
 Best Local Similarity 24.0%; Pred. No. 7.6;
 Matches 72; Conservative 24; Mismatches 90; Indels 114; Gaps 16;

Qy 3 ARRSORRG-----RRGPGTALLVPLALGLALACGLLLA 40
 Db 32 ARRRRRGGSDAITVAELTGEIPIRDHGHAGDPAHASGPAANGR----- 79
 Qy 41 VVSLGSRASLSAQEPAQBELVAEE-----DQDPSELNPQTESQDPAPFLNLRVPR 92
 Db 80 -VQGEAAPQSPAEVPAEQ-VAEEPTRTVYNSQPEPRPKPPQDRREGSELSYPRPL 137
 Qy 93 R-----SAPGKRKTRARRAI---AAHY-----EVHPRPQDQ----- 121
 Db 138 RHTSDRAPAGPPSGAEHMSDPDVEHYDPLVDLTVGEAEAEVTEVRAQPGRGHERHA 197
 Qy 122 --AQAGVDGTSGWEEARINSS-----PLRYNRQIGEIFIVR-----AGLYLYICQV 167
 Db 198 AAAAGTDEGGGAARVARRALDVPFLNR---GALVLIQSILAVAFGALF-----I 249
 Qy 168 HFDE--GKAVYKLKDL-----LVDSGLALRCLEEFSA-----AASLIGPOLRLCQ 211
 Db 250 AFDQLWRNNSIVALVLSVMVILGLVSVRAVRKTDIASTLIYAVAGALITLGP-LALLQ 308

RESULT 13

T30604
 hypothetical protein 3L - Molluscum contagiosum virus 1
 N:Alternate names: MC003L
 C:Species: Molluscum contagiosum virus 1
 C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
 C:Accession: T30604
 R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
 Science 273, 813-816, 1996
 A>Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
 A:Reference number: 220876; MUID:96325459; PMID:8670425
 A:Accession: T30604
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-445 <SEN>
 A:Cross-references: EMBL:U60315; PIDN:AAC55131.1
 C:Genetics:
 A:Note: MC003L

Query Match 6.9%; Score 87; DB 2; Length 445;
 Best Local Similarity 22.1%; Pred. No. 12;
 Matches 56; Conservative 31; Mismatches 86; Indels 80; Gaps 12;

Qy 18 TALLVPLALGLALACGL-----LLAVVSLGSRASLSAQEPAQ 57
 Db 3 TALLCALA-----ALCCLSTEQRKRGDGVGVSVRHSWNESVHVVNGEDVTLCARQHTS 57
 Qy 58 EELVAEE-----DQDPSELNPQTESQ-----DPAPFLNLRVPR-----RSEA 95
 Db 58 ESVOQADYIALYVFRPENTVEEYLSRSPFTHGSHSLSDPGPW---LIDDDDIWROSV 114
 Qy 96 PKGKTRAR-----RAIAAHYEVHPR-----PQDGAQAGVDGTSGWBEARINSSSPLRYN 147
 Db 115 QRANRSHRLDQLDILLVQYVMGEMITIPNHDGSHFCL-----THRWNSA----- 160
 Qy 148 RQIGEFIVR-----AGLYLYICQVHFDEGKAVYKLDLLVDGVLALRCLEEFSAATASS 202
 Db 161 -ELGCWLTRVTTDDVGYYVFWKPHNETAVATILRLDLVLRPRVTVSASFATEDTC 219
 Qy 203 LQPQLRLCOVSGL 215
 Db 220 V--VVLTKVSGL 230

RESULT 14

B75346
 Probable competence protein ComEC/Rec2 - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: B75346
 R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75346
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-755 <WHI>
 A:Cross-references: GB:AE002025; GB:AE000513; NID:g6459627; PIDN:AAF11405.1; PID:g64596
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1854
 A:Map position: 1

Query Match 6.8%; Score 86.5; DB 2; Length 755;
 Best Local Similarity 26.7%; Pred. No. 23;
 Matches 51; Conservative 14; Mismatches 41; Indels 85; Gaps 10;

Qy 8 RRRGRGEPG-TALLVPLALG-----LGLALACGL--LLAVVSL- 44
 Db 23 RRRGHRAEAGRLAWPLPLALGIGGIGWQLGLGWAAPVLLIIGAALALLDARPLIALALL 82
 Qy 45 -----GSRASLSAQEPAQ-----EELVAEEDQDPSELNPQTESQDP 81
 Db 83 GGGLGYGS-AHLQAREPDRIAPWIGALVLRGHWGDFLTDPEFKARVALAPKPGQGE 141
 Qy 82 APFLNLRVPR--RR-----SAPGKRTRA-----RR 105
 Db 142 VVAGRLIRPDGRIRPGFPDQAAWLSRQGLLVPTPKAVLRAEVKKHVPBERGLRGHFR 201
 Qy 106 AIAAHYEVHPR 116
 Db 202 GLSAH--LSPR 210

RESULT 15

E98121
 hypothetical protein clpC-truncation [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
 C:Accession: E98121
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
 Y, P.; Sun, P.M.; Winkler, M.E.

Search completed: April 12, 2003, 08:40:10
Job time : 26 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:14 ; Search time 12 Seconds
(without alignments)
860.634 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARRSRRRRGRGEPGTAL.....PWAHLKAAPFLTYFGLFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	249	1 TN12_HUMAN	O43508 homo sapien
2	1020	80.4	225	1 TN12_MOUSE	O45907 mus musculus
3	109.5	8.6	272	1 TNF5_CHICK	Q91808 gallus gall
4	108.5	8.6	260	1 TNF5_CANFA	Q97626 canis famil
5	95.5	7.5	201	1 TNFB_MACEU	Q9xt48 macropus eu
6	95.5	7.5	254	1 TNF9_HUMAN	P41273 homo sapien
7	91.5	7.2	240	1 TN14_HUMAN	O43557 homo sapien
8	90	7.1	441	1 CG22_ANTMA	F34801 antirrhinum
9	90	7.1	707	1 JIPI_MOUSE	Q9wv19 mus musculus
10	87	6.9	137	1 TNFB_RABIT	F10154 oryctolagus
11	87	6.9	204	1 TNFB_BOVIN	Q06600 bos taurus
12	87	6.9	291	1 TN10_MOUSE	P50592 mus musculus
13	87	6.9	310	1 Y497_MYCTU	O11162 mycobacteri
14	86.5	6.8	250	1 TNFC_MACEU	Q9xt47 macropus eu
15	86	6.8	139	1 YQFB_BACSU	P54467 bacillus su
16	86	6.8	205	1 TNFB_MARMO	Q9jmo9 marmota mon
17	85	6.7	372	1 LMXB_MOUSE	O88609 mus musculus
18	85	6.7	379	1 LMXB_HUMAN	O60663 homo sapien
19	84.5	6.7	933	1 VGLB_HSV1	O04453 herpesvirus
20	84	6.6	310	1 TNFC_MARMO	Q9jml0 marmota mon
21	83.5	6.6	885	1 VGLB_HSV2S	F24994 herpes simp
22	83	6.5	228	1 BIOD_PSEAE	Q9i614 pseudomonas
23	83	6.5	936	1 PHL1_YEAST	P39521 saccharomyc
24	82	6.5	258	1 RL2_ARATH	P46286 arabidopsis
25	82	6.5	369	1 LMXB_MESAU	O60554 mesocricetu
26	82	6.5	844	1 PHSG_DROME	Q9xt19 drosophila
27	81.5	6.4	260	1 RL2_TOBAC	F25998 nicotiana t
28	81.5	6.4	260	1 TNF5_FELCA	Q97605 felis silve
29	81	6.4	244	1 TNFC_HUMAN	O06643 homo sapien
30	81	6.4	273	1 OSAS_BOBUB	Q09089 borrelia bu
31	80.5	6.3	250	1 TN13_HUMAN	O75888 homo sapien
32	80.5	6.3	281	1 TN10_HUMAN	P50591 homo sapien
33	80.5	6.3	675	1 PRTS_BOVIN	P07224 bos taurus

RESULT 1
TN12_HUMAN
ID TN12_HUMAN STANDARD; PRT; 249 AA.
AC O43508; Q8MUZ7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 12 (TNF-related weak inducer of apoptosis) (TWEAK) (APO3 ligand).
GN TNFSF12 OR APO3L OR DR3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_taxid=9606;
OX [1]
RN SEQUENCE FROM N.A., AND N-TERMINUS OF SOLUBLE FORM.
RP TISSUE=Tonsil, and Fetal liver;
RC MEDLINE=98070415; PubMed=9405449;
RX Chicheportiche Y., Bourdon F.R., Xu H., Huu Y.-M., Scott H., Hession C., Garcia I., Browning J.L.;
RA "TWEAK, a new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis."
RT J. Biol. Chem. 272:32401-32410(1997).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal kidney;
RC MEDLINE=98228355; PubMed=9560343;
RX Marsters S.A., Sheridan J.P., Pitti R.M., Brush J., Goddard A., Ashkenazi A.;
RA "Identification of a ligand for the death-domain-containing receptor Apo3."
RT Curr. Biol. 8:525-528(1998).
RL [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Tonsil;
RC Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RN FUNCTION.
RP PubMed=10085077;
RA Lynch C.N., Wang Y.C., Lund J.K., Chen Y.-W., Leal J.A., Wiley S.R.;
RC "TWEAK-induces angiogenesis and proliferation of endothelial cells."
RL J. Biol. Chem. 274:8455-8459(1999).
CC -!- FUNCTION: Binds to FN14 and possibly also to TNFRSF12/APO3. Weak inducer of apoptosis in some cell types. Mediates NF-kappaB activation. May promote angiogenesis and the proliferation of endothelial cells.
CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, pancreas, skeletal muscle, brain, colon, small intestine, lung, ovary, prostate, spleen, lymph node, appendix and peripheral blood lymphocytes. Low expression in kidney, testis, liver, placenta, thymus and bone marrow. Also detected in fetal kidney, liver, lung and brain.
CC -!- PTM: The soluble form derives from the membrane form

34 80.5 6.3 928 1 VGLB_HSVBP P17471 bovine herp
35 80.5 6.3 932 1 VGLB_HSVBC P12640 bovine herp
36 80.5 6.3 1565 1 DMN_HUMAN O15061 homo sapien
37 80 6.3 547 1 RM56_HUMAN P83111 homo sapien
38 80 6.3 664 1 UL47_HSV1F P08313 herpes simp
39 80 6.3 693 1 UL47_HSV1L P10231 herpes simp
40 79.5 6.3 241 1 TN13_MOUSE Q9d777 mus musculus
41 79.5 6.3 814 1 CADF_HUMAN P55291 homo sapien
42 79.5 6.3 4466 1 DYHC_ANTCR P39057 anthocidari
43 79 6.2 261 1 TNFS_AOTTR Q9bdm3 actus trivi
44 79 6.2 261 1 TNFS_CALJA Q9bdm3 callithrix
45 79 6.2 280 1 TNF6_MACMU Q9my16 macaca mula

ALIGNMENTS

CC by proteolytic processing.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 125.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF030099; AAC51923.1; -
 CC EMBL; AF055872; AAC39724.1; -
 CC EMBL; BC019047; AAH19047.1; ALT_FRAME.
 CC Genew; HGNC:11927; TNFSF12.
 CC MIN; 602695; -
 CC InterPro; IPR000478; TNF_family.
 CC Pfam; PF00229; TNF; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; FALSE_NEG.
 CC PROSITE; PS50049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 CC CHAIN 1 249
 CC TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC MEMBER 12, MEMBRANE FORM.
 CC TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC MEMBER 12, SECRETED FORM.
 CC CYTOPLASMIC (POTENTIAL).
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC CLEAVAGE.
 CC N-LINKED (GLCNAC...).
 CC E660843361C28EBA CRC64;
 CC SEQUENCE 249 AA; 27216 MW; 5660843361C28EBA CRC64;
 CC
 CC Query Match 100.0%; Score 1268; DB 1; Length 249;
 CC Best Local Similarity 100.0%; Pred. No. 1.8e-99;
 CC Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 MAARSRRRRGRRGPGTALLVPLALGGLACGLALLVVLGSLASLSAQEPQSEL 60
 CC Db 1 MAARSRRRRGRRGPGTALLVPLALGGLACGLALLVVLGSLASLSAQEPQSEL 60
 CC
 CC Qy 61 VAEEDQDSELPNQPTEESQDPAPFLNRLVRRSRAPKGRKTRARRAIAAHVEVHPRPQD 120
 CC Db 61 VAEEDQDSELPNQPTEESQDPAPFLNRLVRRSRAPKGRKTRARRAIAAHVEVHPRPQD 120
 CC
 CC Y 121 GAQAGVDTGVSWEARINSSPLRYNQIGEFIVTRAGLYLYCQVHFDEGKAVYLKLD 180
 CC Db 121 GAQAGVDTGVSWEARINSSPLRYNQIGEFIVTRAGLYLYCQVHFDEGKAVYLKLD 180
 CC
 CC Qy 181 LLDVGVLRCLLEESATASLSGQPLRLCQVSGLLARPGSSLRITLPAHLKAAPFL 240
 CC Db 181 LLDVGVLRCLLEESATASLSGQPLRLCQVSGLLARPGSSLRITLPAHLKAAPFL 240
 CC
 CC Qy 241 TYFGLFQVH 249
 CC Db 241 TYFGLFQVH 249
 CC
 CC RESULT 2
 CC ID TN12 MOUSE STANDARD; PRT; 225 AA.
 CC AC 054907; Q9CTP2;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Tumor necrosis factor ligand superfamily member 12 (TNF-related weak
 CC inducer of apoptosis) (TWEAK) (Fragment).
 CC GN TNFSF12.
 CC OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal macrophage;
 RX MEDLINE=98070415; PubMed=9405449;
 RA Chicheportiche Y., Bourdon P.R., Xu H., Hsu Y.-M., Scott H.,
 RT Hession C., Garcia I., Browning J.L.;
 RT "TWEAK, a new secreted ligand in the tumor necrosis factor family that
 RT weakly induces apoptosis.";
 RL J. Biol. Chem. 272:32401-32410(1997).
 RN [2]
 RP SEQUENCE OF 83-225 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Azakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontseki S.,
 RA Hayaehizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Binds to FN14 and possibly also to TNFRSF12/AP03. Weak
 CC inducer of apoptosis in some cell types. Promotes angiogenesis and
 CC the proliferation of endothelial cells. Mediates NF-KappaB
 CC activation (By similarity).
 CC -1- SUBUNIT: Homotrimer (Potential).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- PTM: The soluble form is produced from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF030100; AAC53517.1; -
 CC EMBL; AK020909; BAB32249.1; -
 CC MGD; MGI:1196259; Tnfsf12.
 CC InterPro; IPR000478; TNF_family.
 CC Pfam; PF00229; TNF; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; FALSE_NEG.
 CC PROSITE; PS50049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 CC NON TER 1 1
 CC CHAIN <1 225 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC MEMBER 12, MEMBRANE FORM.
 CC CHAIN 70 225 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 CC MEMBER 12, SECRETED FORM (BY SIMILARITY).
 CC TRANSMEM <1 21 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 22 225 EXTRACELLULAR (POTENTIAL).
 CC SITE 69 70 CLEAVAGE (BY SIMILARITY).

[illegible]

[illegible]

PFam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF; 1; FALSE_NEG.
 DR PROSITE; PS00049; TNF; 2; 1.
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
 KW Alternative splicing.
 CHAIN 1 240
 FT CHAIN 283 240 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 283 240 MEMBER 14, MEMBRANE FORM.
 FT CHAIN 283 240 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 283 240 MEMBER 14, SOLUBLE FORM.
 FT CHAIN 283 240 CYTOPLASMIC (POTENTIAL).
 FT CHAIN 283 240 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
 FT CHAIN 283 240 (POTENTIAL).
 FT CHAIN 283 240 EXTRACELLULAR (POTENTIAL).
 FT CHAIN 283 240 CLEAVAGE (POTENTIAL).
 FT CHAIN 283 240 POTENTIAL (GLCNAC...).
 FT CHAIN 283 240 MISSING (IN ISOFORM 2).
 FT CHAIN 283 240 L -> V (IN REF. 4).
 FT CHAIN 283 240 E -> K (IN REF. 2).
 FT CHAIN 283 240 CONFLICT 214 214
 FT CHAIN 283 240 SEQUENCE 240 AA; 26351 MW; 490867E1390B39 CRC64;
 Query Match 7.2%; Score 91.5; DB 1; Length 240;
 Best Local Similarity 25.0%; Pred. No. 1;
 Matches 44; Conservative 18; Mismatches 47; Indels 67; Gaps 7;
 QY 5 RSRRG-RRCEPTGALLVPLALGGLALCLGLLLAVVSLGSRASLSAQPAQEEELVAE 63
 DB 26 KSHRRQSCSVARVGLGLL-LMGAGLAVQVWFLQLHRLG-----EWV-- 69
 QY 64 EDQDPSELNPQTESQDPAPFLNLRPRRSGPKRTRARRAIAAHYVHPRCQDGAQ 123
 DB 70 -----TRLPDGPAGSWEQLIQERS-----HEVNPAAHLTCAN 102
 QY 124 AGVDGTVSGWEARINSSPLRYNRQI-----GFIVTRAGLYLYYQV 167
 DB 103 SSLTG-----SGPFLMETQLGLAFGLRGLSYHDGALVTVTKAGYYIYSKV 147
 RESULT 8
 CG22 ANTMA STANDARD; PRT; 441 AA.
 AC P34801;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G2/mitotic-specific cyclin 2.
 S Antirrhinum majus (Garden snapdragon).
 S Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
 OX NCBI_TaxID=4151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94148008; PubMed=8313906;
 RA Robert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
 RT "Patterns of cell division revealed by transcriptional regulation of
 genes during the cell cycle in plants";
 RL EMOB J. 13:616-624(1994).
 CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
 AND ARE ABRUPTLY DESTROYED AT MITOSIS.
 CC -!- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM
 A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
 IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 ABRUPTLY DESTROYED AT MITOSIS.
 CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X76123; CAB53729.1; -
 DR FIR; S41710; S41710.
 DR HSSP; P30274; IVIN.
 DR InterPro; IPR004366; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Mitosis.
 SQ SEQUENCE 441 AA; 49205 MW; E6E4C037C98880A7 CRC64;
 Query Match 7.1%; Score 90; DB 1; Length 441;
 Best Local Similarity 23.8%; Pred. No. 2.8;
 Matches 67; Conservative 42; Mismatches 102; Indels 70; Gaps 14;
 QY 1 MAARRSQRR-----RGRGEPGTALLVPLALGGLALCLGLL----- 38
 DB 26 MAYEKNRRALGDIGNVTVRGVEKALPOVSRPITRGF-----CAQLIANAEAAAAENN 80
 QY 39 ---LAVVSLGSRASLS-----AQEPAQEELVAEEDQDPSELNPQTESQDPAPFLNLR 90
 DB 81 KNSLAVNAKAGDGLPIKAVARVPVQKTKVSKPOEIIIEISPDTEKKK--APVLEKEIT 138
 QY 91 PRRS-----APKGRKTRARRAIAAHYVHPRPGO-----DGAQAGVDGTVSGWEE----- 135
 DB 139 GEKSLKKKALTLSTLTARSKAASV-VRTAPKEQIVDIDADVNDLAVVEYEDMYKFY 197
 QY 136 -ARINSSPLRY---NRQGEFIVTRAGLYLYYQVIFD---EGKAVYKLDLLVDGVL 188
 DB 198 KSAENDSRPHDYMSQPEINEKM--RAILLDLVQVHYKFEELSPETLYLTIN-IVDRYLA 254
 QY 189 LRC-----LEEFSAATASLGPQLRCLQVSGLLALRPGS 222
 DB 255 SKTTSRRELQGLGSSMLIASKEYEINWAPEVNDLVCIISDGS 295
 RESULT 9
 JIPI_MOUSE STANDARD; PRT; 707 AA.
 ID JIPI_MOUSE
 AC Q9WV19; Q9WV18; Q9WV17; Q9RIH9; Q9RIZ1; Q35145;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-jun-amino-terminal kinase interacting protein 1 (JNK-interacting
 protein 1) (JIP-1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1)
 DE (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1).
 GN MAPK8IP1 OR PRKM8IP OR Jip1 OR IB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM JIP-1A), AND POSSIBLE FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=97382313; PubMed=9235893;
 RA Dickens M., Rogers J.S., Cavanagh J., Raitano A., Xia Z.,
 RA Halpern J.R., Greenberg M.E., Sawyers C.L., Davis R.J.;
 RT "A cytoplasmic inhibitor of the JNK signal transduction pathway";
 RL Science 277:693-696(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS JIP-1B; JIP-1C; JIP-1D AND JIP-1E).
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=99196470; PubMed=10098834;
 RA Kim I.-J., Lee K.-W., Park B.Y., Lee J.-K., Park J., Choi I.Y.,
 RA Eom S.-J., Chang T.-S., Kim M.J., Yeom Y.I., Chang S.K., Lee Y.-D.,
 RA Choi E.-J., Han P.-L.;
 RT "Molecular cloning of multiple splicing variants of JIP-1

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CC the Eu

DR MGD;

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CC EMBL; Z77162; CAB00923.1; -;
 DR EMBL; AE006952; AAK44740.1; -;
 DR TIGR; MT0517; -;
 DR Tuberculin; Rv0497; -;
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 231 251 POTENTIAL.
 FT TRANSMEM 257 277 POTENTIAL.
 FT TRANSMEM 286 306 POTENTIAL.
 FT DOMAIN 33 39 POLY-ARG.
 FT DOMAIN 197 202 POLY-ALA.
 FT SEQUENCE 310 AA; 33092 MW; 4954027F694DF5C2 CRC64;

Query Match 6.9%; Score 87; DB 1; Length 310;
 Best Local Similarity 24.0%; Pred. No. 3.3;
 Matches 72; Conservative 24; Mismatches 90; Indels 114; Gaps 16;

3 ARSQRRG-----RRGPGTALLVPLALGLGLALACLGLLLA 40
 |||:||||
 32 ARRRRRRGSDAITVAELTGEIPIIRDDHHGPDAAHASQSPAANG----- 79
 41 VVSLGSRASLSAQPAQELVAEE-----DODSELNPQTEESODPAPFLNRLVRPR 92
 |||:||||
 80 -VQGEAAPQSPAPVAEQ-VAEPRTVYWSQPEPRPKSPQDRRESGPELSEYRPL 137
 |||:||||
 93 R-----SAPGKRKTRARRAI---AAHY-----EVHPRQDQ----- 121
 |||:||||
 138 RHTSDRAPAGPPSGAEHMSDPVEHYPDLDVLDTEVGEAAETEVREAQPCGRGHA 197
 |||:||||
 122 --AAGVDGTVSGWEHARINSS-----PLRYNRQIGEIFIVR-----AGLYLYLCQV 167
 |||:||||
 198 AAAAAGTDEGDAEAAVARRALDVVETLWR---GALVLIQSILAVAFAGLGF-----I 249
 |||:||||
 168 HFDE---GKAVYLLKLDL---LVGDVLALRCLEEFSAF-----AASLGLPQLRLCQ 211
 |||:||||
 250 AFDQLWRNSIVALVLSVMVILGLVSVRAVRKTEDIASTLIAVAVGALITLGP-LALLQ 308
 |||:||||

RESULT 14
 TNFC_MACEU
 ID TNFC_MACEU STANDARD; PRT; 250 AA.
 AC QXAT47;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 J Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
 DE necrosis factor ligand superfamily member 3).
 GN LTB OR TNFSP3 OR TNFC.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Harrison G.A., Cooper D.W., Deane E.M.;
 RT "cDNA sequence of the tamar wallaby lymphotoxin beta chain.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytokine that binds to LTRP/TNFSF3. May play a specific
 CC role in immune response regulation. Provides the membrane anchor
 CC for the attachment of the heterotrimeric complex to the cell
 CC surface.
 CC -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
 CC (less prevalent) two LTA and one LTB subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL; AF119337; AAD41774.1; -;
 DR HSSP; P01374; ITNR.
 DR InterPro; IPR003636; TNF abc.
 DR InterPro; IPR00478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
 KW CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1 26 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 27 47 (POTENTIAL).
 FT DOMAIN 48 250 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 250 AA; 26143 MW; AD37FB975452FE84 CRC64;

Query Match 6.8%; Score 86.5; DB 1; Length 250;
 Best Local Similarity 21.2%; Pred. No. 2.8;
 Matches 65; Conservative 31; Mismatches 95; Indels 115; Gaps 12;

QY 1 MAARRSQRRGRGEGCTALLVPLALGLALACLGLLAWSLGSRASLSAQEPAQEEL 60
 |||:||||
 DB 1 MGAPGUETRAG--GPNKSYLLUASVG-----AAVLGTLISVPIVTLVLAIMPQGGQ 54
 |||:||||
 QY 61 VAEEDDDPS-----ELNPQTEESQDPAPFLNRLVRPRSPAKGRKTRARRAI 107
 |||:||||
 DB 55 VA---DPSGPGQLLQQLGFHKLPEVESRDLSPIPAAHLIGAKSSHGLR----- 102
 |||:||||
 QY 108 AAHYEVHPRQDGAQAGVDGTVSGWEHARINSSPLRYNRQIGEIFIVTRAGLYLYCQV 167
 |||:||||
 DB 103 -----WVSGYEAFKSGT--QFLGDEGLLALPDQGIYFLYCHI 139
 |||:||||
 QY 168 HF-----DEGKAVYLLKLDLVDGVLAALRCLEEFSAFATAASSLG-PQLRL- 209
 |||:||||
 DB 140 GYGRAPSGGEGQFRSQAGDPGVPTLSSQL-----FRAGASGSEPELQLQ 186
 |||:||||
 QY 210 -----CQVSGLLALRPSSLRITLPLWAHLKAAPF---LTY 242
 |||:||||

DB 187 GFETVTPPVQHARGVGQGLWYATVGFGLVQLRGGEKIYVNV---SHLELVDFRRGKTF 243
 |||:||||
 QY 243 FGLFQV 248
 |||:||||
 DB 244 FGAVMV 249

RESULT 15
 YQFB_BACSU
 ID YQFB_BACSU STANDARD; PRT; 139 AA.
 AC P54467;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 GN Hypothetical protein yqfb.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=97124195; PubMed=8969508;
 RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
 RA Kobayashi Y.;
 RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
 RT the Bacillus subtilis genome containing the skin element and many

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 12, 2003, 08:38:15 ; Search time 32 Seconds
(without alignments)

1603.304 Million cell updates/sec

Title: US-09-905-810-2

Perfect score: 1268

Sequence: 1 MAARRRRRRRRGEPCTAL.....PWAHLKAAPLTYFGULFQVH 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 671580 seqs, 206047115 residues

al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	116	9.1	325	5	Q9V5G2	Q9V5G2 drosophila
2	97	7.6	643	16	Q9K217	Q9K217 streptomyc
3	95	7.5	375	16	Q9RRH5	Q9RRH5 deinococcus
4	94	7.4	937	16	Q93JDI	Q93JDI streptomyc
5	93.5	7.4	776	16	Q9RJ01	Q9RJ01 streptomyc
6	93	7.3	378	16	Q9AAB9	Q9AAB9 caulobacter
7	92.5	7.3	707	11	Q925J8	Q925J8 mus musculu
8	92	7.3	977	4	Q8TEN1	Q8TEN1 homo sapien
9	91.5	7.2	212	16	Q86312	Q86312 mycobacteri
10	90.5	7.1	1100	2	Q937L3	Q937L3 deinococcus
11	89	7.0	522	10	Q9FTN7	Q9FTN7 oryza sativ
12	89	7.0	664	16	Q9HYT9	Q9HYT9 pseudomonas
13	89	7.0	854	16	Q9E2P0	Q9E2P0 streptomyc
14	88	6.9	655	16	Q9FBR7	Q9FBR7 streptomyc
15	87.5	6.9	274	10	Q949L6	Q949L6 beta vulgar
16	87.5	6.9	5192	2	Q93TW9	Q93TW9 stigmatella

17	87	6.9	267	2	Q24793	Q24793 borrelia ga
18	87	6.9	273	2	Q44962	Q44962 borrelia bu
19	87	6.9	273	2	Q31376	Q31376 borrelia ga
20	87	6.9	427	10	Q8S9W3	Q8S9W3 oryza sativ
21	87	6.9	445	12	Q98174	Q98174 molluscum c
22	87	6.9	565	16	Q9KV66	Q9KV66 streptomyc
23	86.5	6.8	225	13	Q9IB42	Q9IB42 paralicthy
24	86.5	6.8	308	4	Q96M87	Q96M87 homo sapien
25	86.5	6.8	331	10	Q942P9	Q942P9 oryza sativ
26	86.5	6.8	536	4	Q9HB96	Q9HB96 homo sapien
27	86.5	6.8	755	16	Q9RTB1	Q9RTB1 deinococcus
28	86.5	6.8	810	16	Q97N72	Q97N72 streptococc
29	86	6.8	287	13	Q90WT9	Q90WT9 gallus gall
30	86	6.8	614	4	Q8WU14	Q8WU14 homo sapien
31	86	6.8	855	4	Q9NYK9	Q9NYK9 homo sapien
32	86	6.8	878	4	Q9UFU7	Q9UFU7 homo sapien
33	86	6.8	1294	5	Q9GY29	Q9GY29 leishmania
34	86	6.8	1837	5	Q967R4	Q967R4 caenorhabdi
35	85.5	6.7	361	4	Q9BQ88	Q9BQ88 homo sapien
36	85.5	6.7	412	4	Q8WY10	Q8WY10 homo sapien
37	85	6.7	272	2	Q31374	Q31374 borrelia ga
38	85	6.7	431	10	Q23088	Q23088 arabidopsis
39	84.5	6.7	402	2	Q51973	Q51973 pseudomonas
40	84.5	6.7	450	16	Q8Y1A3	Q8Y1A3 ralstonia s
41	84.5	6.7	748	5	Q8T2Y0	Q8T2Y0 trypanosoma
42	84.5	6.7	9376	2	Q8S168	Q8S168 pseudomonas
43	84	6.6	260	10	Q9SD27	Q9SD27 arabidopsis
44	84	6.6	274	2	Q45194	Q45194 borrelia ga
45	84	6.6	532	4	Q96AP3	Q96AP3 homo sapien

ALIGNMENTS

RESULT 1

Q9V5G2 PRELIMINARY; PRT; 325 AA.

AC Q9V5G2; AC Q9V5G2; (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CG12919 protein.

GN CG12919.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos L.G.,

Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Chert J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobaraj C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M., M.G.,
 RA Palazolo M., Pittman G.S., Fan S., Pollard J., Furi V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirakak R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF58848.1; --
 DR FlyBase; FBgn0033483; CG12919.
 DR InterPro; IPR000478; TNF_family.
 DR SMART; SM00207; TNF; 1.
 PROSITE; PS00251; TNF; 1; 1.
 PROSITE; PS50049; TNF; 2; 1.
 SQ SEQUENCE 325 AA; 35862 MW; 685CCB69694FlA3A CRC64;

Query Match 9.1%; Score 116; DB 5; Length 325;
 Best Local Similarity 25.4%; Pred. No. 0.029;
 Matches 57; Conservative 32; Mismatches 97; Indels 38; Gaps 10;

QY 47 RASLSAQEPAQEELVAE-----EDQPSSELNQTESQDPAPFLNR-----LVRPR 92
 DB 118 KRSRSIADVRNEEQINQHTLEQKSEATSKES--PAPLHRRRHHSHRLLVRKG 175
 QY 93 RSAPKGRKTRARRAIAAHVEHPRPGDGAQAGVDGTSGWEARINSSPLRYNRQIGE 152
 DB 176 ESLLSARSEDSP--AAHFLSSRRRHQSGM-GYHGMVIGNDNERNYSYQG-HQTRDGV 231
 QY 153 FIVTRAGLYLYYLCVQV-----HFDEKAVYLKDLLVDGVLALRCLEEFSAATAASLGQQL 207
 DB 232 LTVNTGLYVYAQICYNNSHQNGFVFE-----QGDTPFLQCLN-----TVPTNMPKV 281
 QY 208 RLCQVSGLLALRPOSSLRIRTL---PWAHLKAAPLTYFGLFOV 248
 DB 282 HTCHTSGLIHLERNRIHLKDINHNDNAVLREGNRSYFGIFKV 325

RESULT 2

Q9KZ17 PRELIMINARY; PRT; 643 AA.
 Q9KZ17;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein SC02220.
 GN SC02220 OR SC1087.15.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RC Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser I., Lark L., Murphy L., Oliver K., O'Neil S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2).";

RL Nature 417:141-147(2002).
 DR EMBL; AL355752; CAB90868.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 643 AA; 66537 MW; 1217A5C8E3CD419 CRC64;
 Query Match 7.6%; Score 97; DB 16; Length 643;
 Best Local Similarity 24.4%; Pred. No. 3.3;
 Matches 54; Conservative 21; Mismatches 102; Indels 44; Gaps 6;
 QY 25 ALGLGALACLGLLAVVSLGSRASLSAQEPAQEELVAEEDQPSSELNQTESQDPAPF 84
 DB 227 ALVAGRALVCGALLGPGDGAAPPAQNPAAEAALDPGRLTKAAPAAWETSAR 286
 QY 85 LNLVRRPRRSGKGRKTRARRAIAAHVEHPRPGDGAQAGVDGTSGWEARINSSPL 144
 DB 287 TDFSVMFARGGLTGDELLRALLA-----VWARPGESVGVSATPTGATG-----GP- 332
 QY 145 RYNRQIGEFIVTRAGLYLYYLCVQVHFDEKAVYLKDLLVDGVLALRCLEEFSAATASSL- 203
 DB 333 -----AGPPOLLYAGEVDTARVV-----VLHGLRLVRVAEPKDGSAALD 374
 QY 204 -----GPQLRLCQVSGLLALRPGSSLRIRTLFWAHLKAA 237
 DB 375 PARTDGAAGRAATAVVLG-----RADGNVRYLTAPWVTKAAA 411

RESULT 3

Q9RRH5 PRELIMINARY; PRT; 375 AA.
 ID Q9RRH5
 AC Q9RRH5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein DR2516.
 GN DR2516.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RC MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002081; AAF12062.1; --
 DR TIGR; DR2516; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 375 AA; 39596 MW; 197B39785ED30B3 CRC64;

Query Match 7.5%; Score 95; DB 16; Length 375;
 Best Local Similarity 23.9%; Pred. No. 2.5;
 Matches 64; Conservative 26; Mismatches 76; Indels 102; Gaps 12;

QY 4 RRSORRRGRGEGPT--ALLVPLALGIALGIALACUGLLAVVSLGSRASLSAQE-PAQEEL 60
 DB 24 RRPGRAPGRGQPGSHPAARQRLRADLGAALA-----LVADVVTREPLPAGELTLLDL 77
 QY 61 VAEDQPSSELNQTESQDPAPFLNLRPRRSGKGRKTRARRAIAAHVEHPR-PGQ 119
 DB 78 AR-----QDLESDDSP-----TDLAVQARATFRLPGD 108
 QY 120 DGAQAG--VDGTSGWEARINSSPLRYNRQIGE-----FIVTRAGLYLY----- 164
 DB 109 PGAGFGHPISGTLAGLE--RLSAASLRAHWARFQGRGSLGVGVADADAQEVYELVAGLFA 166

DB	122	YDRQIGFTVIRAGLYLYCQVHFDGKAVYLKDLVNGVLALRCLEBFSATASSPGP	181
QY	206	QLRLCQVSGLLALPGSSLRIRTLPAHLKAAPFLTYFGLFQVH	249
DB	182	QLRLCQVSGLLALPGSSLRIRTLPAHLKAAPFLTYFGLFQVH	225
RESULT 6			
US-09-813-329-6			
; Sequence 6, Application US/09813329			
; Patent No. US20020012968A1			
; GENERAL INFORMATION:			
; APPLICANT: Bristol-Myers Suibb Company			
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole			
; TITLE OF INVENTION: Variants Thereof			
; FILE REFERENCE: D0016.dp			
; CURRENT APPLICATION NUMBER: US/09/813,329			
; CURRENT FILING DATE: 2001-03-20			
; PRIOR APPLICATION NUMBER: 60/190,816			
; PRIOR FILING DATE: 2000-03-21			
; NUMBER OF SEQ ID NOS: 65			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 6			
; LENGTH: 409			
; TYPE: PRT			
; ORGANISM: Drosophila melanogaster			
US-09-813-329-6			
Query Match 9.1%; Score 116; DB 10; Length 409;			
Best Local Similarity 25.5%; Pred. No. 0.011;			
Matches 56; Conservative 33; Mismatches 95; Indels 36; Gaps 10;			
QY	47	RASLSAQEPAQEELVAE---EDQDPSLNPQTEESODPAPFLNRLVRRRSAPKGRKTR	102
DB	208	RKSRSTADVNEQNTQGHTELOEKSSNEATSKES--PAPLHHR-----RRMHSRRHLL	261
QY	103	ARRA-----IAAHYEVHPRPGDGAQGVDTGVSQWEEARINSSSPLRYNRQIGFIYV	156
DB	262	VRKARGEDSRPAAPHLLSRRRRHOGSM-GYHGDYIGNDNERNYSYQG-HFQTRDGVLTVT	319
QY	157	RAGLYLYCOV-----HFDEGKAVYLKDLVDGVLAALRCLEBFSATASSLGPQLRLCQ	211
DB	320	NTGLYVYVYQAICYNNSHDQNGFTVF-----QGDTPFLQCLN---TVPTNMPHKVHTCH	369
QY	212	VSGLLALPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV	248
DB	370	TSGLIHLERNERHLKDIHNDRNAVLREGNRSYFGIFKV	409
RESULT 7			
US-09-813-329-4			
; Sequence 4, Application US/09813329			
; Patent No. US20020012968A1			
; GENERAL INFORMATION:			
; APPLICANT: Bristol-Myers Suibb Company			
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole			
; TITLE OF INVENTION: Variants Thereof			
; FILE REFERENCE: D0016.dp			
; CURRENT APPLICATION NUMBER: US/09/813,329			
; CURRENT FILING DATE: 2001-03-20			
; PRIOR APPLICATION NUMBER: 60/190,816			
; PRIOR FILING DATE: 2000-03-21			
; NUMBER OF SEQ ID NOS: 65			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 4			
; LENGTH: 406			
; TYPE: PRT			
; ORGANISM: Drosophila melanogaster			
US-09-813-329-4			
Query Match 8.3%; Score 105.5; DB 10; Length 406;			
Best Local Similarity 24.2%; Pred. No. 0.11;			


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Matches 54; Conservative 35; Mismatches 97; Indels 37; Gaps 10;

QY 49 SLSAQEPAQEEL-----VABEDQ----DPSEL-----NPQTEESQDPAPFLNRLVRPRR 93
Db 198 SYNAAKKKQERKSRIADVREBNIQGNHTLQEKSSNEATSKRMHSRRHLVVRKE 257
QY 94 SAPKGRKTRARRAIAAHVEVHPRPGDGAQAGVDGTGSGWEARINSSSPLRYNRQIGEF 153
Db 258 SLLSARGSDSRP--AAHPHLSRRRHQSGM-GYHGDMYIGNDNERNYSQG-HFQTRDGVL 313
QY 154 IVTRAGLYYLXCOV-----HFDEGKAVYKLDDLVDGVLAALRCLEEPSATAASSILGPOLR 208
Db 314 TVTNTGLYYVYAQQCYNNSHOQNGFIVF-----QGDTPTFLQCLN---TVPTNMPHKVH 363
QY 209 LCVQSGLIALRFGSSLIRTL---PWAHLKAAPFLTYYFGLFOV 248
Db 364 TCHTSGLIHLERNERIHLKDINHDRNAVLREGNRSYFGIFKV 406

--SULT 8
-09-813-329-2
Sequence 2, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Subb Company
TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor C
TIME OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813.329
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 409
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-813-329-2

Query Match      8.2%; Score 104; DB 10; Length 409;
Best Local Similarity 25.9%; Pred. No. 0.14;
Matches 56; Conservative 32; Mismatches 100; Indels 28; Gaps 10;

QY 47 RASLSAQEPAQOEELVAE---EDQDPSELNPQTEESQDPAPP-LNRLVPRRSAPKGRKT 101
Db 208 RKRSIADVRNEEQNIQGNHTLQEKSSNEARKSES--PALHLRRMRHSRRHLVVRKA 265
102 RARRA-IAAHVEVHPRPGDGAQAGVDGTGSGWEARINSSSPLRYNRQIGEFIVTRAGL 160
Db 266 RSEDSRPAAHPHLSRRRHQESM-GYHGDMY-IENDRCSYQGHFQTRDGVLTVTNAGL 323
QY 161 YLYLCOV-----HFDEGKAVYKLDDLVDGVLAALRCLEEPSATAASSILGPOLR 215
Db 324 YYVYAQIWGYNSHOQNGFIVF-----QGDTPTFLQCLN---TVPTNMPHKVHTCSTGL 373
QY 216 LALRPGSSLIRTL---PWAHLKAAPFLTYYFGLFOV 248
Db 374 IHLERNERIHLKDINHDRNAVLREGNRSYFGIFKV 409

RESULT 9
US-09-027-287-39
Sequence 39, Application US/05027287A
Patent No. US20020064869A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
TITLE OF INVENTION: Apoptosis Inducing Molecule II
FILE REFERENCE: 1488.0650004
CURRENT APPLICATION NUMBER: US/09/027.287A
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; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-027-287-39

Query Match      7.3%; Score 92.5; DB 10; Length 208;
Best Local Similarity 25.0%; Pred. No. 0.62;
Matches 41; Conservative 18; Mismatches 38; Indels 67; Gaps

Qy 22 VPLA-LGLGIALACLGLLAV-----VSLGSRASLSAQEPAQELVAEDQDFSELNPQT 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 IPRAVGLGLLLLMGAGLAVQGWFLQLHLRLG-----EMV-----T 38

Qy 76 EESQDPAPFLNRLVPRSPAPKGRKTEARRAIAAHYEVHPRQDGAQAGVCGTVSGWEE 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 39 RLPDGRAGSWEQIQIERRS-----HEVNPAAHLTGANSLSLTG-----T 38

Qy 136 ARINSSSPFLRYNRQI-----GEEIVTRAGLYLYLCQV 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 ----SCGFLLEWETQLGLAFURGLSYHDGALVVTKAGYYIYSKV 115

RESULT 10
US-09-252-656B-39
; Sequence 39, Application US/09252656B
; Patent No. US20020081647A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.0650006
; CURRENT APPLICATION NUMBER: US/09/252,656B
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-656B-39

Query Match      7.3%; Score 92.5; DB 10; Length 208;
Best Local Similarity 25.0%; Pred. No. 0.62;
Matches 41; Conservative 18; Mismatches 38; Indels 67; Gaps

```


APPLICANT: Ruben, Steven M.
APPLICANT: Zhang, Jun
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.0650006
CURRENT APPLICATION NUMBER: US/09/252,656B
CURRENT FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: US 60/075,409
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/027,287
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/003,886
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 08/822,953
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/013,923
PRIOR FILING DATE: 1996-03-22
PRIOR APPLICATION NUMBER: US 60/030,157
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-252-656B-2

Query Match 7.2%; Score 91.5; DB 10; Length 240;
Best Local Similarity 25.0%; Pred. No. 0.93; Mismatches 47; Indels 67; Gaps 7;
Matches 44; Conservative 18;
QY 5 RSQRERG-RRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEELVAE 63
DB 26 RSHRRQSCSVARVGLGLLL-LMGAGLAVQGWFLLOLHWRLG-----EMV-- 69
QY 64 EDQDPSLNQTEESQDPAPFNLRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGDGAQ 123
DB 70 -----TRLPDGPGAGSWEQLIQERRS-----HEVNPAAHLTGAN 102
QY 124 AGVDGTVSGWEERINSSPLRYNRQI-----GEFIVTRAGLYLYCOV 167
DB 103 SSLTG-----SGPFLWETQLGLAFRLGLSYHDGALVVTKAGYIIYSKV 147

RESULT 15
US-10-066-209-4
Sequence 4, Application US/10066209
Patent No. US2002011510A1
GENERAL INFORMATION:
APPLICANT: Brigham-Burke, Michael R.
APPLICANT: Young, Peter R.
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2
FILE REFERENCE: GH-50030-D1
CURRENT APPLICATION NUMBER: US/10/066,209
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/072,993
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 240
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-10-066-209-4

Query Match 7.2%; Score 91.5; DB 12; Length 240;
Best Local Similarity 25.0%; Pred. No. 0.93; Mismatches 47; Indels 67; Gaps 7;
Matches 44; Conservative 18;
QY 5 RSQRERG-RRGEPGTALLVPLALGLGLALACLGLLAVVSLGSRASLSAQEPAQEELVAE 63
DB 26 RSHRRQSCSVARVGLGLLL-LMGAGLAVQGWFLLOLHWRLG-----EMV-- 69
QY 64 EDQDPSLNQTEESQDPAPFNLRLVRRPSAPKGRKTRARRAIAAHYEVHPRPGDGAQ 123
DB 70 -----TRLPDGPGAGSWEQLIQERRS-----HEVNPAAHLTGAN 102
QY 124 AGVDGTVSGWEERINSSPLRYNRQI-----GEFIVTRAGLYLYCOV 167
DB 103 SSLTG-----SGPFLWETQLGLAFRLGLSYHDGALVVTKAGYIIYSKV 147

Search completed: April 12, 2003, 08:47:28
Job time : 18 secs

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QY 165 -----COMFHDEKAVYKLDLLVDGVLALRCLLEFSATASSLGPQLRLCOVYS-- 213
DB 167 DWQGEDRPMFAHFGPLRLHL-----PSATGQTHLSLVAPG 204
QY 214 -----GLLALRGSSLRIT 228
DB 205 PGRDPDPLWQALTAALSGGSASRLFT 232

RESULT 4
Q93JDI PRELIMINARY; PRT; 937 AA.
AC Q93JDI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative membrane protein.
GN STBAC16H6.31 OR SC05996 OR SCBAC16H6.31.
Streptomyces coelicolor.
OX Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]_TaxID=1902;
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Collins M.R., Harris D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
Kinsahi H., Hopwood D.A.;
RX MEDLINE=97000351; PubMed=8843436;
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AL596162; CAC44610.1;
DR InterPro; IPR000408; Reg_chromat_condens.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 13.
DR PROSITE; PS00626; RCC1_2; UNKNOWN 1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 5.
DR PROSITE; PS00082; WD_REPEATS_2; 9.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 937 AA; 98790 MW; F14E4478A6B6B2F5 CRC64;

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Query Match

Best Local Similarity 7.4%; Score 94; DB 16; Length 937;

Matches 46; Conservative 19; Mismatches 64; Indels 52; Gaps 6;

```

QY 5 RSORRRGRGEPOTALLVPLALGLALALCLGLLLAVSLGSRASLSAQEP-----A 56
DB 213 RSEGLDRTRNLRTARIVATLGCGLLVAS---TLSVAVLSRAEATRQDQAVVOOLIT 269
QY 57 QEELVAEEQDPSLNPQTEESQDPAP-----FLNRLVPRRS-----APKG 98
DB 270 QSSLLAERDPFAARLKALAARIDPSPETRFVAVLDAAVNPASGVLSHVPVDSVAFSPDG 329
QY 99 R-----KTRARRAIAAHE-----VHPRQDGAQAGVDCGTGVSQWEE 135
DB 330 RTVASGSDGVVRWRTGTQRTAGRPLIGHHQGITSIAFAPDGTLLASSGFGDTGLVMDL 389
QY 136 A 136
DB 390 A 390

RESULT 5
Q9RJ01 PRELIMINARY; PRT; 776 AA.
AC Q9RJ01;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative cation-transporting ATPase.
GN SCO0164 OR SCU1.13.
OX Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]_TaxID=1902;
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
Kinsahi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL109962; CABS3131.1;
DR InterPro; IPR00106; AATRNA_ligaseII.
DR InterPro; IPR001757; ATPase_E1-E2.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PROSITE; PS00339; AA TRNA_LIGASE II 2; UNKNOWN 1.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN 1.

```

SEQUENCE 776 AA; 80626 MW; 3E2C4D66D24ECB7D CRC64;

Query Match 7.4%; Score 93.5; DB 16; Length 776;
Best Local Similarity 24.1%; Pred. No. 8.5;
Matches 63; Conservative 30; Mismatches 103; Indels 65; Gaps 11;

OY 12 RRGEGCTALLVPLALGLGALA--CLGILLA-VVSLGRSASLSAQEPQAEELVAEEQQDP 68
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 73 RRHAGVDIIVLALGGTLAGVEYLAVGIATLMLATGRTLEGAAQRASHDLHALLAHAP 132

OY 69 SELNPQTEESQDPAPFLNLRPRRSAPKGRKRTRARRAJAAHYEVHPRPQCQDGAQAQVDG 128
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 133 RSARRITGG-----VVR---VPLSEITAGDALVVGPGEVVP-----VDG 169

OY 129 TVSGWE---EARINSSSPRYNRQICE----FIVTRAGLYLYLCQVHFDEGKAYVKLDL 181
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 170 RVESTEAVILDESVLITQEPLQVTRQREGARGAVNAGGAFDL-----RATAIEQDS 220

OY 182 LVDGVIALRCLEFSATAASSLGPOURLCO-----VSGLLARPGSSLR---- 225
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 221 TYAGIVRL-----AQAGAESAPVVRLLADRYAAWFLPALATAALAWLVGSRAVAV 274

OY 226 -IRTLPAHLKAAPFLTYFGL 245
: : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 275 LVVATPCPLLAAAPVAVVUGL 295

RESULT 6

OXAAB9 PRELIMINARY; PRT; 378 AA.

AC OXAAB9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hlyd family secretion protein.
GN CC0683.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
[1]

RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblum T.V., Laub M.R.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A.S., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Whinn M.L., Haft D.H.,
Kotlony J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Uttrechtack T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005743; AKZ22668.1; -.
DR InterPro; CO0683; -.
DR InterPro; IPR003997; RctD.
DR PRINTS; PR01490; RTXTOXIND.
KW Complete proteome.
SQ SEQUENCE 378 AA; 39659 MW; 88B818C437C15CBC CRC64;

Query Match 7.3%; Score 93; DB 16; Length 378;
Best Local Similarity 25.6%; Pred. No. 3.8;
Matches 68; Conservative 28; Mismatches 98; Indels 72; Gaps 12;

OY 9 RRGRR--GEFGTALLVPLALGLGALACIGLLAVSVISGRASLSAQEPA--QEELVAE 63
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 50 REGDRVVGQPIATLTLSALEGGDSFAVLSR-----SLGAQSSARGSRAAATQAALAE 104

OY 64 EDODPSSELNPQTEESQDPAPFLNLRPRRS--APKGRKTRAR-----RATAIAHYEVHP 115
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 105 SRQ-----LTORRALNLRELAERSLALOTERLTLLAREAVARAETIAAQGFSLP 154

OY 116 RFGQPZAQAQVDGTVSGWEEAFINSSSPRYNRQIQEGFIVTRAGLYLYLCQVHFDEGKAV 175

Db	155	RE----	LQARRSAELAVQOEASTLSQALSVERQIGEV-----	DARLA	193
Qy	176	YKLDL---	LVDGVLALRCLEFSAASSIGPOLRLCQVSGLLA-----		217
Db	194	APIDLQARAARAAEASTLAGLEQ-QATQVEAQGRYVVVATVAGRVAALPVEAGQTGVGVAA	252		
Qy	218	---	LRPGSSLRIRTLFWAHLKAAPFL	240	
Db	253	VAVLTGDSALVAEL-YAPSAAGFV	277		
RESULT 7					
ID	Q925J8	PRELIMINARY;	PRT;	707	AA.
AC	Q925J8;				
DT	01-DEC-2001	(TrEMBLrel. 19, Created)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DE	DE	Protein kinase mitogen-activated 8 interacting protein.			
GN	MAPK8IP OR PRKM8IP.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RP	[1]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=ILS;				
RA	Eringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,				
RA	Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;				
RT	"High-Throughput Sequence Identification of Gene Coding Variants				
RT	within Alcohol-Related QTLs."				
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF332076; AAK56104.1; -.				
DR	MCD; MGI:1309464; Mapk8ip.				
DR	InterPro; IPR000050; PID_domain.				
DR	InterPro; IPR001452; SH3.				
DR	Pfam; PF00640; PID; 1.				
DR	Pfam; PF00018; SH3; 1.				
DR	PROSITE; PS01179; PID; 1.				
DR	PROSITE; PS50002; SH3; 1.				
KW	Kinase.				
SEQ	SEQUENCE	707	AA; FDS53D891B6F5AA6	CRC64;	
Query Match 7.3%; Score 92.5; DB 11; Length 707;					
Best Local Similarity 23.3%; Pred. No. 9.3;					
Matches 48; Conservative 19; Mismatches 76; Indels 63; Gaps					
Qy	1	MAARRSRRRGRRGPGTALLVPLALG-----	LGLALA	33	
Db	1	MAERESGLGRGAAPPAASPFLGLHIATSPNFRFLTHDISLEEFEDDLSEITDECGISLQ	60		
Qy	34	C-----LGL-----LLAVVSLGSRASLSAQPAQEELV-----	AEEDQD-----	67	
Db	61	CKDTLSLRPPRAGLSAGSGSAGSRLOAQMQLDIDAAGDTFGADDEDEDEDELLAAQ	120		
Qy	68	-PSELNPQTEESQDPAPFLNLRVRRSAP---KGRKTRARRAIAAAHYEVHPRGQDGAQ	123		
Db	121	RLQGVPPKAEENQDPAP-----RSQGGFGTSGDGYRPRKRTTLNLPQVPRSQDTLN	174		
Qy	124	AGVDGTVSGWEARINSSPLRYNRQ	149		
Db	175	NNSLGKHSWQDRVSRSSSLKTKGEQ	200		
RESULT 8					
ID	Q8TET1	PRELIMINARY;	PRT;	977	AA.
AC	Q8TET1;				
DT	01-JUN-2002	(TrEMBLrel. 21, Created)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DE	FLJ00093	protein (Fragment).			

```

RA Parkhill J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayar L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uutterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; Z93777; CAB07841.1; -.
DR EMBL; AE007002; AAK45514.1; -.
DR TIGR; T1257; -.
DR Tuberculist; Rv1219c; -.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; tetR; 1.
KW DNA-binding; Hypothetical protein; Transcription regulation;
KW Complete proteome.
SQ SEQUENCE 212 AA; 23181 MW; 8FBC03B909EA88C0 CRC64;

Query Match 7.2%; Score 91.5; DB 16; Length 212;
Best Local Similarity 24.5%; Pred. No. 2.5;
Matches 53; Conservative 26; Mismatches 78; Indels 59; Gaps

QY 11 GRGEGCTALLVPLALGGLG-----ALACLGILLAVVSLGSRASLSAQPAQBELVAEE-- 64
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 21 GRHG-----FGVGLRAIAEAGVSAALVTHHFGSKEGL---RKACDDFVAEEIR 66
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 65 -----DQPSLNPQTEESQDPAPFLNRLVPRRSAPKGRKTRARRAIAAHVEVHPR 116
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 67 SSKAAALKNDPTTWLAQWAEIESYAPLMAYLVRSWSGGELAKMLWQMI----- 117
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 117 PGDGAQAGVDGTGVCWEERINSSSPLRYNQIGEFI-VTRAGLYLYLCQVHFD----- 170
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 118 ---DNAEEYLD-----EGVRAGTVKPSRDPRARARFLAITGGGFLLYLQMHNPDTLR 168
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 171 -----EGKAVYLKDLLVDGVGLARCL-EEFSATA 199
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
DB 169 AALRDYAHDMVLPSLEVYTEGLLDAMYEAFIAEA 204
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:

RESULT 10
Q937L3 PRELIMINARY; PRT; 1100 AA.
AC Q937L3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SMC protein.
GN SMC.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
[1]
RN RP SEQUENCE FROM N.A.
RA Cobbe N., Heck M.M.S.;
RT "Phylogenetic analysis of SMC proteins";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417688; CAD10418.1; -.
DR InterPro; IPR003439; ABC transportr.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02483; SMC_C; 1.
DR Pfam; PF02463; SMC_N; 1.
SQ SEQUENCE 1100 AA; 118812 MW; 9800A26EFB71BC2F CRC64;

Query Match 7.1%; Score 90.5; DB 2; Length 1100;

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ID	Q9HVT9	PRELIMINARY;	PRT;	664 AA.
AC	Q9HTI9;			
AD	01-WAR-2001 (TrEMBLrel. 16, Created)			
AT	01-MAR-2001 (TrEMBLrel. 18, Last sequence update)			
DT	01-OCT-2001 (TrEMBLrel. 16, Last annotation update)			
DT	01-NAR-2001 (TrEMBLrel. 18, Last annotation update)			
DT	Hypothetical protein PA3305.			
DN	PA3305.			
GE	Pseudomonas aeruginosa.			
OS	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas.			
OC	Pseudomonas.			
ON	NCBI_TaxID=287;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=ATCC 15692 / PA01;			
RC	MEDLINE=2043737; PubMed=10984043;			
RC	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.			
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou			
RA	Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.			
RA	Brody R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.			
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,			
RA	Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;			
RT	"Complete genome sequence of Pseudomonas aeruginosa PA01, an			
RT	opportunistic pathogen."			
RL	Nature 406:959-964(2000).			
DR	EMBL; AE004753; AAC06693.1; --			
KW	Hypothetical protein; Complete proteome.			
SK	SEQUENCE 664 AA; 73136 MW; 19EBBEF3098D1F4E CRC64;			
Query Match 7.0%; Score 89; DB 16; Length 664;				
Best Local Similarity 26.0%; Pred. No. 18;				
Matches 70; Conservative 26; Mismatches 109; Indels 64; Gaps				
QY	10 RGRGEPGTALLVPLALGLGLALACGLLLAVVLSGSRASLSAQEPAGEE-----LVAE			
DB	224 RGRRAGALALLRDLSSL-----LRTARGVARQARLSEEBERRVERWLAALASAL			
QY	64 EQDPSLNPQTESQDPAPFLNRLVPRSPKPKETPARPAIAAHVEVHPFGQDGAQ			
DB	276 EGTDPASQALRELAQVA-----VEPQMSNDQ-RYLLTRCSVLLLKAVN-----AAE			
QY	124 AGVDGTVSGWEARINSSPLRYNR--QIGEFIVTRAGL-----VYLY-----			
DB	322 KGNRAVASGEVGRVSGAGTSLSHRDQLQWALFVGTISALALLGLSVIYITAWPAASGM			
QY	165 -----CQHFDEGKAVYKLDLLVDGVLAALRCLEEFSAATASSIGPOLRCQVSG--LL			
DB	382 LLAAVVCSLFANRDNAVAIGLSFLRGIVYAI-----PAAMLVVSQWLLPQWNGFPFL			
QY	217 ALRPGSSLRIRTLPAWHLKAAPLITYFGL 245			
DB	433 *CLAMGVPLFFATLGNVAPVPTAGTATSFAT 461			
RESULT 13				
ID	Q9F2P0	PRELIMINARY;	PRT;	854 AA.
AC	Q9F2P0;			
AD	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-WAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Putative ABC transport system integral membrane protein.			
OS	Sc30110 OR SCE41.19C			
OS	Streptomyces coelicolor.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomycineae; Streptomyces			
OX	NCBI_TaxID=1902;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3(2);			
RA	Saunders D.C., Harris D.;			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
RP	[2]			
RP	SEQUENCE FROM N.A.			

RESULT	ID	Q9FBR7	PRELIMINARY;	PRT;	655 AA.
AC	Q9FBR7;	01-MAR-2001	(TReMBLrel. 16, Created)		
DC	Q9FBR7;	01-MAR-2001	(TReMBLrel. 16, Last sequence update)		
DT	DT	01-JUN-2002	(TReMBLrel. 21, Last annotation update)		
DE	DE		Putative ion chelataase.		
DN	SC05278	OR SCCB12.	02.		
GN	Streptomyces	coelicolor.			
OC	Bacteria;	Firmicutes;	Actinobacteria;	Actinobacteridae;	
OC	Actinomycetales;	Streptomycineae;	Streptomycetaceae;	Streptomycetes.	
OX	NCBI_TaxID=1902;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A3(2) / M145;				
RC	Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,				
RA	Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,				
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,				
RA	Cronin A., Fraser A., Goble A., Hidaigo J., Hornsby T., Howarth S.,				

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Query Match          6.9%; Score 87.5; DB 10; Length 274;
Best Local Similarity 28.9%; Pred. No. 8;
Matches 26; Conservative 12; Mismatches 43; Indels 9; Gaps

QY 48 ASLSAQE-PAQELVAEDQD-----PSLNPTQTESQDPAPFLNRLVRRPSAPKG 98
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 82 AAVEAENTPVQSEAKTEKEEAPAAENTPAQEEPKTDEDOQTPAEEPAAPAAHSAAPA 141
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 99 RKTRARRAIAAHYEVHPRGQGAQGVGD 128
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 142 EEHQAAEQPAAAPVAEHHPAAEQPAAAPAAIDG 171
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Search completed: April 12, 2003, 08:40:50
Job time : 38 secs

CC activators or agonists, are used to treat a deficit of TREPA, e.g. to
 CC promote wound healing or tissue grafting, by promoting vascularisation,
 CC also to induce apoptosis for treating cancer and eliminating autoreactive
 CC T cells, as an adjunct to cancer chemotherapy or antiviral treatment.
 CC TREPA peptides can also be used to target cytotoxic agents or for
 CC affinity isolation of the corresponding receptor, the nucleic acid for
 CC which can be used to transform tumour cells to render them more
 CC responsive to TREPA and to screen for TREPA mimics.
 CC Ribozymes, antisense RNA, antibodies or peptides, are used to treat
 CC TREPA-associated diseases, e.g. tumours and metastases (by inhibiting
 CC vascularisation), inflammation or a wide range of autoimmune conditions,
 CC conditions involving abnormal stimulation of epithelial cells (e.g.
 CC atherosclerosis), for birth control (inhibiting ovulation and placental
 CC formation) or other angiogenic conditions (e.g. ulcers).
 XX Sequence 189 AA;

Query Match 62.5%; Score 792; DB 19; Length 189;
 Best Local Similarity 99.3%; Pred. No. 1.1e-71;
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 97 KGRKTRARRAIAAHYEVHPRGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 156
 DB 37 KGRKTRARRGIAAHYEVHPRGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 96
 QY 157 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLAALRCLEEFSAATAASSLGPQLRLCQVSGLL 216
 DB 97 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLAALRCLEEFSAATAASSLGPQLRLCQVSGLL 156
 QY 217 ALRPGSSLRIRTLPAWHLKAAAPFLTYFGLFQVH 249
 DB 157 ALRPGSSLRIRTLPAWHLKAAAPFLTYFGLFQVH 189

RESULT 14
 AAE00892
 ID AAE00892 standard; Protein; 189 AA.
 XX AC AAE00892;
 XX DT 04-JUL-2001 (first entry)
 XX DE Human UL4flag TREPA soluble construct.
 XX KW Human; tumour necrosis factor; TNF; angiogenesis; wound healing; tumour;
 KW TREPA; TNF related endothelium proliferative agent; metastasis; grafting;
 KW vulnary; HUVEC; human umbilical vein endothelial cell; UL4flag.

Homo sapiens.
 AA US6207642-B1.
 PN XX
 XX DT 27-MAR-2001.
 PD XX
 XX DT 26-JUN-1998; 98US-0105343.
 XX PF 12-FEB-1997; 97US-0798692.
 XX PR 10-FEB-1998; 98US-0021706.
 XX PA (ABBO) ABBOTT LAB.
 XX PI Wiley SR;
 XX DR WPI; 2001-280760/29.

XX Inducing angiogenesis in mammal at desired sites for promoting wound
 XX healing, by administering soluble fragment of extracellular domain of
 XX tumor necrosis factor related endothelium proliferative agent protein
 XX -
 XX Example 2; Column 75-78; 53pp; English.
 XX The present invention relates to extracellular signal molecules,

CC particularly members of tumour necrosis factor (TNF) family molecules
 CC designated as TREPA (TNF related endothelium proliferative agent).
 CC Soluble biologically active TREPA are used to treat TREPA-associated
 CC diseases, tumours or metastases. TREPA is used for inducing angiogenesis
 CC in human for promoting wound healing and for vascularising grafted
 CC tissue for successful grafting and to promote tissue grafts. The present
 CC amino acid sequence is human UL4flag TREPA soluble construct. This
 CC sequence which is a biologically active molecule is capable of inducing
 CC proliferation in HUVEC (human umbilical vein endothelial cells).
 XX Sequence 189 AA;

Query Match 62.5%; Score 792; DB 22; Length 189;
 Best Local Similarity 99.3%; Pred. No. 1.1e-71;
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 97 KGRKTRARRAIAAHYEVHPRGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 156
 DB 37 KGRKTRARRGIAAHYEVHPRGQDGAQAGVDGTVSGWEARINSSPLRYNRQIGEIFVT 96
 QY 157 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLAALRCLEEFSAATAASSLGPQLRLCQVSGLL 216
 DB 97 RAGLYLYLCQVHFDEGKAVYKLDLLVDGVLAALRCLEEFSAATAASSLGPQLRLCQVSGLL 156
 QY 217 ALRPGSSLRIRTLPAWHLKAAAPFLTYFGLFQVH 249
 DB 157 ALRPGSSLRIRTLPAWHLKAAAPFLTYFGLFQVH 189

RESULT 15
 AAE00895
 ID AAE00895 standard; Protein; 146 AA.
 XX AC AAE00895;
 XX DT 04-JUL-2001 (first entry)
 XX DE Human TREPA (TNF related endothelium proliferative agent) fragment.
 XX KW Human; tumour necrosis factor; TNF; angiogenesis; wound healing;
 KW TREPA; TNF related endothelium proliferative agent; tumour; metastasis;
 KW grafting; vulnary.

Homo sapiens.
 OS US6207642-B1.
 PN XX
 XX DT 27-MAR-2001.
 XX PF 26-JUN-1998; 98US-0105343.
 XX PR 12-FEB-1997; 97US-0798692.
 XX PR 10-FEB-1998; 98US-0021706.
 XX PA (ABBO) ABBOTT LAB.
 XX PI Wiley SR;
 XX DR WPI; 2001-280760/29.

XX Inducing angiogenesis in mammal at desired sites for promoting wound
 XX healing, by administering soluble fragment of extracellular domain of
 XX tumor necrosis factor related endothelium proliferative agent protein
 XX -
 XX Example 14; Fig 1; 53pp; English.
 XX The present invention relates to extracellular signal molecules,
 XX particularly members of tumour necrosis factor (TNF) family molecules
 XX designated as TREPA (TNF related endothelium proliferative agent).
 XX Soluble biologically active TREPA are used to treat TREPA-associated
 XX diseases, tumours or metastases. TREPA is used for inducing angiogenesis
 XX in human for promoting wound healing and for vascularising grafted

CC tissue for successful grafting and to promote tissue grafts.
CC The present amino acid sequence is human TREPA fragment.

XX
SQ Sequence 146 AA;
Query Match 60.0%; Score 761; DB 22; Length 146;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 RRATAAHVEVHPRPGDGAQAGVDGTSGWEERINSSPLRYNRQIGEFIVTRAGLYYL 163
Db 1 RRATAAHVEVHPRPGDGAQAGVDGTSGWEERINSSPLRYNRQIGEFIVTRAGLYYL 60
Qy 164 YCOVHDEGKAVYLKLDLLVDGVLALRCLEEFSAATAASSLGQPLRLCOVSGLLALRPSS 223
Db 61 YCOVHDEGKAVYLKLDLLVDGVLALRCLEEFSAATAASSLGQPLRLCOVSGLLALRPSS 120
Qy 224 LRIRLTPWAHLKAAPFLTYFGLFOVH 249
nb 121 LRIRLTPWAHLKAAPFLTYFGLFOVH 146

Search completed: April 12, 2003, 08:39:00
Job time : 38 secs

```

RT sporulation genes."
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Goughly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue J.C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
CC Nature 390:249-256(1997).
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; D84432; BA012474.1; --
CC EMBL; Z99117; CAB14479.1; --
CC Subtilisin; BGI1652; YqfB.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 3 23 POTENTIAL.
SQ SEQUENCE 139 AA; 15740 MW; 60C7F38CDB1F4CB7 CRC64;
-----
Query Match 6.8%; Score 86; DB 1; Length 139;
Best Local Similarity 27.8%; Pred. No. 1.6;
Matches 30; Conservative 18; Mismatches 46; Indels 14; Gaps 3;
QY 33 ACGLGLLAVSVLSAQEPAQEELVAEEDDPSELNPTQESQD--PAPELNLVR 90
DB 13 ALIGLISAIFGKSK-----EKQNSQKRRKPOHVOSAPQKKSKEDAPAPIENRMVQ 66
QY 91 PRSAPKGRKTRAR-----RAIAAHYEHVPRPGQDGAQAGVDGTSG 132
DB 67 ARREAERRETARNLKGLELDLAAAKQKTVYTKQKMLQYNKDTVVQS 114

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Search completed: April 12, 2003, 08:39:19
Job time : 15 secs

15-JUN-2002 (Rel. 41, Last annotation update)
 Lymphotoxin-alpha precursor (LTA-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
 LTA OR TNFSF1 OR TNFB.
 GN Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91065534; PubMed=2249779;
 RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V., Andreyeva A.V., Nedospasov S.A.;
 RT "Cloning and structural analysis of genes coding for tumor necrosis factor and lymphotoxin in rabbits.";
 RL Mol. Biol. (Mosk) 23:1743-1750(1989).
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane protein (heterotrimers) (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC
 CC EMBL; X55745; CAA39275.1; ALT_SEQ.
 CC EMBL; M60340; AAA31483.1; -.
 CC EMBL; M60341; AAA31485.1; -.
 CC PIR; JH0309; JH0309.
 CC PIR; P00098; P00098.
 CC HSSP; P01374; 1TNR.
 CC InterPro; IPR003636; TNF_abc.
 CC InterPro; IPR000478; TNF_family.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PS01234; TNECROSISCT.
 CC ProDom; PD002012; TNF_abc; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF 1; 1.
 CC PROSITE; PS0049; TNF 2; 1.
 CC Cytokine; Glycoprotein; Cytotoxin; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 197 LYPHOTOXIN-ALPHA.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 197 AA; 21126 MW; 0CF18CC90B5E2345 CRC64;
 Query Match 6.9%; Score 87; DB 1; Length 197;
 Best Local Similarity 23.7%; Pred.No. 1.9;
 Matches 61; Conservative 24; Mismatches 82; Indels 90; Gaps 11;
 QY 16 PGTALLVPLALGIGLALACGLGLLVVSLGSLASLQAQEP-----AQBELVAEEDQDPS 69
 DB 3 PPGRLVPL-----LLGLLLAPPFGAQLPGAEFPSPSARNAQRL--QKHFGHS 51

QY 70 ELPNQTESQDPAPFLNRLVRRRSAPKGRKTRAR--RAIAAHYEVHPRPGDGAQAGVD 127
 DE factor ligand superfamily member 1).
 DB 52 TLKPAALVGD-----SAQDSLWRANTDRAFLRH----- 82
 QY 128 GTVSGWEARINSSPLRYNRQIGEFIVTRAGLYLYCYQVHFD-EG---KAVYKLKDLLV 183
 DE Lymphotoxin-alpha precursor (LTA-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
 DB 83 -----GFSLSNNSLLVPSGLYFVYSQVVFSGEGSPKAVPTPLYLAAH 125
 QY 184 DGVLAALRCLEEFSA-----TAASSL-----GPOLRLCQVSGLLALRPGSSLRITL 229
 DE factor ligand superfamily member 1).
 DB 126 E-----VOLFSQVSHFVPLLSAQKSCVCGPGPWRVSYQCAVELLTQGDLSHTD 178
 QY 230 PWAHLKAAPFLTYFGLF 246
 DB 179 GIAHLLSPSSVFFGAF 195
 RESULT 11
 TNFB BOVIN STANDARD; PRT; 204 AA.
 AC Q06600;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lymphotoxin-alpha precursor (LTA-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
 RT "Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.";
 RL Cytokine 5:336-341(1993).
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane protein (heterotrimers) (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC
 CC EMBL; Z14137; CAA78510.1; -.
 CC PIR; S24641; S24641.
 CC HSSP; P01374; 1TNR.
 CC InterPro; IPR003636; TNF_abc.
 CC InterPro; IPR000478; TNF_family.
 CC Pfam; PF00229; TNF; 1.
 CC PRINTS; PS01234; TNECROSISCT.
 CC ProDom; PD002012; TNF_abc; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF 1; 1.
 CC PROSITE; PS0049; TNF 2; 1.
 CC Cytokine; Glycoprotein; Cytotoxin; Signal.
 FT SIGNAL 1 33
 FT CHAIN 34 204 LYPHOTOXIN-ALPHA.

RT preferentially expressed in brain.";

RL J. Neurochem. 72:1335-1343(1999).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM JIP-1B), AND CHARACTERIZATION.

RC TISSUE=Brain;

RX MEDLINE=99422004; PubMed=10490659;

RA Yasuda J., Whitmarsh A.J., Cavanagh J., Sharma M., Davis R.J.;

RT "The JIP group of mitogen-activated protein kinase scaffold

RT proteins.";

RT Mol. Cell. Biol. 19:7245-7254(1999).

RN [4]

RP TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.

RX MEDLINE=20177638; PubMed=10712642;

RA Pellet J.-B., Haefliger J.-A., Staple J.K., Widmann C., Welker E.,

RT Hirling H., Bonny C., Nicod P., Catsicas S., Waerber G., Riederer B.M.;

RT "Spatial, temporal and subcellular localization of islet-brain 1

RT (IB1), a homologue of JIP-1, in mouse brain.";

RL Eur. J. Neurosci. 12:621-632(2000).

RN [5]

RP INTERACTION WITH LRPS.

RX MEDLINE=20400498; PubMed=10827173;

RA Gotthardt M., Trommsdorff W., Nevitt M.F., Shelton J.,

RT Richardson J.A., Stockdorf W., Nimpf J., Herz J.;

RT "Interactions of the low density lipoprotein receptor gene family with

RT cytosolic adaptor and scaffold proteins suggest diverse biological

RT functions in cellular communication and signal transduction.";

RL J. Biol. Chem. 275:25616-25624(2000).

RN [6]

RP FUNCTION.

RX MEDLINE=21446505; PubMed=11562351;

RA Whitmarsh A.J., Kuan C.-Y., Kennedy N.J., Kelkar N., Haydar T.F.,

RA Moraes J.P., Appel M., Rossini A.A., Jones S.N., Flavell R.A.,

RA Rakic P., Davis R.J.;

RT "Requirement of the JIP1 scaffold protein for stress-induced JNK

RT activation.";

RL Genes Dev. 15:2421-2432(2001).

CC -I- FUNCTION: The JNK-interacting protein (JIP) group of scaffold

CC proteins selectively mediates JNK signaling by aggregating

CC specific components of the MAPK cascade to form a functional JNK

CC signaling module. JIP1 is required for JNK activation in response

CC to excitotoxic stress. Cytoplasmic JIP1 causes inhibition of JNK-

CC regulated activity by retaining JNK in the cytoplasm and by

CC inhibiting the JNK phosphorylation of c-Jun. May also participate

CC in Apoptosis-specific reelin signaling. Directly, or indirectly,

CC regulates Glut2 gene expression and beta-cell function (By

CC similarity). Appears to have a role in cell signaling in mature

CC and developing nerve terminals.

CC -I- SUBUNIT: Forms homo- or heterooligomeric complexes. Binds specific

CC components of the JNK signaling pathway namely JNK, MAPKK7 and

CC MLK2, MKK3 and DLK. Also binds the proline-rich domain-containing

CC splice variant of apolipoprotein E receptor 2 (ApoER2). Binds the

CC TPR motif-containing C-terminal of kinesin light chain. Interacts,

CC via the PID domain, with rhoGEF (By similarity). Binds the

CC cytoplasmic tails of LRPI and LRPI2 (Megalin).

CC -I- SUBCELLULAR LOCATION: Cytoplasmic. Accumulates in cell surface

CC projections. Under certain stress conditions, translocates to the

CC perinuclear region of neurons. In insulin-secreting cells,

CC detected in both the cytoplasm and nucleus (By similarity).

CC -I- ALTERNATIVE PRODUCTS: 5 isoforms; JIP-1a/1, JIP-1b (shown here),

CC JIP-1c/2a, JIP-1d/2B and JIP-1e/3; are produced by alternative

CC splicing.

CC -I- TISSUE SPECIFICITY: Expressed predominantly in the brain and

CC insulin-secreting cells. In the brain, high expression found in

CC the cerebral cortex and hippocampus. Localizes in the synaptic

CC regions of the olfactory bulb, retina, cerebral and cerebellar

CC cortex and hippocampus. Also expressed in a restricted number of

CC axons, including mossy fibers from the hippocampal dentate gyrus,

CC soma, dendrites and axons of cerebellar Purkinje cells. Also

CC expressed in kidney, testis and prostate. Low levels in heart,

CC ovary and small intestine. Isoform JIP-1b is more predominant in

CC the brain than isoform JIP-1a. JIP-1a is expressed both in the

CC brain and kidney, isoforms JIP-1c, JIP-1d and JIP-1e are brain

CC specific.

CC -I- DEVELOPMENTAL STAGE: Low levels at prenatal stage E15, increased

CC levels during the first postnatal days, with a plateau at

CC postnatal day 15.

CC -I- INDUCTION: Upon neuron differentiation.

CC -I- PTM: Phosphorylated by JNK in differentiated cells.

CC -I- SIMILARITY: BELONGS TO THE JIP SCAFFOLD PROTEINS FAMILY.

CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

CC -I- SIMILARITY: CONTAINS 1 PID DOMAIN.

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CC -----

CC EMBL; AF003115; AAB66317.1; -

CC EMBL; AF109768; AAD38346.1; -

CC EMBL; AF109769; AAD38347.1; -

CC EMBL; AF109770; AAD38348.1; -

CC EMBL; AF109771; AAD38349.1; -

CC EMBL; AF054611; AAD22580.1; -

CC TRANSFAC; T04468; -

CC MGI; MGI:1309464; Prkmbip.

CC InterPro: IPR000050; PID_domain.

CC InterPro: IPR001452; SH3.

CC Pfam; PF00018; SH3; 5.

CC Pfam; PF00640; PID; 5.

CC ProDom; PD000066; SH3; 1.

CC SMART; SM00326; SH3; 1.

CC PROSITE; PS01179; PID; 1.

CC PROSITE; PS50002; SH3; 1.

CC SH3 domain; Alternative splicing; Phosphorylation.

CC FT DOMAIN 41 47 ASP/GLU-RICH (ACIDIC).

CC FT DOMAIN 107 116 JNK/SH3-RICH (ACIDIC).

CC FT DOMAIN 127 281 ASP/SH3-RICH (ACIDIC).

CC FT DOMAIN 355 359 POLY-PRO.

CC FT DOMAIN 484 545 SH3.

CC FT DOMAIN 557 696 PID.

CC FT VARSPPLIC 1 33

CC FT FT

CC FT VARSPPLIC 1 90 MISSING (IN ISOFORM JIP-1E).

CC FT VARSPPLIC 69 93 MISSING (IN ISOFORM JIP-1D).

CC FT VARSPPLIC 558 604 MISSING (IN ISOFORM JIP-1A).

CC FT CONFLICT 144 145 PG -> A (IN REF. 2).

CC FT CONFLICT 593 593 R -> RP (IN REF. 2).

CC SEQUENCE 707 AA; 77281 MW; 274013B12D91049D CRC64;

CC SQ

Query Match 7.1%; Score 90; DB 1; Length 707;

Best Local Similarity 26.5%; Pred. No. 4.9;

Matches 40; Conservative 16; Mismatches 59; Indels 36; Gaps 6;

OY 29 GLALAC---LGL-----LLAVVSLGSRASLSAQEAQELV-----AEDDQD--- 67

DB 56 GISLQCKDTLSLPPRAGLUSAGSSAGSRQLQAEMLQMDLIDAGDTPGAEDEDEED 115

OY 68 -----PSELNPQTEESQDPAPFLNLRPRRSAP---KGRKTRARRAIAHYEVHPRPG 118

DB 116 ELAAQRPGVCPKAEKNQDPAP-----RSQGGPGTSGDGYRKPETTLNLFPPQVPRS 169

OY 119 QDGAQGVDTGVSQWEERINSSPLRYNRQ 149

DB 170 QDTLNNNSLKGKHSWDVRVSRSSSLKGTGEQ 200

RESULT 10

TNFB_RABIT

ID TNFB_RABIT STANDARD; PRT; 197 AA.

AC P10154;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

